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Welcome to STN International! Enter x:x

LOGINID:ssspt189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS	1		Web Page for STN Seminar Schedule - N. America
NEWS	2	JAN 02	STN pricing information for 2008 now available
NEWS	3	JAN 16	CAS patent coverage enhanced to include exemplified prophetic substances
NEWS	4	JAN 28	USPATFULL, USPAT2, and USPATOLD enhanced with new custom IPC display formats
NEWS	5	JAN 28	MARPAT searching enhanced
NEWS	6	JAN 28	USGENE now provides USPTO sequence data within 3 days of publication
NEWS	7	JAN 28	TOXCENTER enhanced with reloaded MEDLINE segment
NEWS	8	JAN 28	MEDLINE and LMEDLINE reloaded with enhancements
NEWS	9	FEB 08	STN Express, Version 8.3, now available
NEWS	10	FEB 20	PCI now available as a replacement to DPCI
NEWS	11	FEB 25	IFIREF reloaded with enhancements
NEWS	12	FEB 25	IMSPRODUCT reloaded with enhancements
NEWS	13	FEB 29	WPINDEX/WPIDS/WPIX enhanced with ECLA and current U.S. National Patent Classification
NEWS	14	MAR 31	IFICDB, IFIPAT, and IFIUIDB enhanced with new custom IPC display formats
NEWS	15	MAR 31	CAS REGISTRY enhanced with additional experimental spectra
NEWS	16	MAR 31	CA/CAPplus and CASREACT patent number format for U.S. applications updated
NEWS	17	MAR 31	LPCI now available as a replacement to LDPCI
NEWS	18	MAR 31	EMBASE, EMBAL, and LEMBASE reloaded with enhancements
NEWS	19	APR 04	STN AnaVist, Version 1, to be discontinued
NEWS	20	APR 15	WPIDS, WPINDEX, and WPIX enhanced with new predefined hit display formats
NEWS	21	APR 28	EMBASE Controlled Term thesaurus enhanced
NEWS	22	APR 28	IMSRESEARCH reloaded with enhancements
NEWS	23	MAY 30	INPAFAMDB now available on STN for patent family searching
NEWS	24	MAY 30	DGENE, PCTGEN, and USGENE enhanced with new homology sequence search option
NEWS	25	JUN 06	EPFULL enhanced with 260,000 English abstracts
NEWS	26	JUN 06	KOREAPAT updated with 41,000 documents
NEWS	27	JUN 13	USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications
NEWS	28	JUN 19	CAS REGISTRY includes selected substances from web-based collections
NEWS	29	JUN 25	CA/CAPplus and USPAT databases updated with IPC reclassification data
NEWS	30	JUN 30	AEROSPACE enhanced with more than 1 million U.S. patent records
NEWS	31	JUN 30	EMBASE, EMBAL, and LEMBASE updated with additional options to display authors and affiliated

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                                organizations
NEWS 32  JUN 30  STN on the Web enhanced with new STN AnaVist
                                Assistant and BLAST plug-in
NEWS 33  JUN 30  STN AnaVist enhanced with database content from EPFULL

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
                                AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

NEWS HOURS      STN Operating Hours Plus Help Desk Availability
NEWS LOGIN      Welcome Banner and News Items
NEWS IPC8       For general information regarding STN implementation of IPC 8

```

Enter NEWS followed by the item number or name to see news on that specific topic.

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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 13:55:21 ON 07 JUL 2008

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:55:47 ON 07 JUL 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0* with SET DETAIL OFF.

=> s Lactobacillus reuteri and toxin(p)bind? and CD4+ cell? and (food or tablet or dietary supplement or confectionery or drug)
0* FILE ADISCTI

=> s Lactobacillus reuteri and toxin(p)bind? and CD4+ cells
0* FILE ADISCTI

=> s Lactobacillus reuteri and toxin(p)bind?

```

0* FILE ADISNEWS
0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
1* FILE BIOTECHABS
1* FILE BIOTECHDS
0* FILE BIOTECHNO
2 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN

```

27 FILES SEARCHED...

```

0* FILE ESBIOWASE
0* FILE FOMAD

```

0* FILE FOREGE
 2* FILE FROSTI
 0* FILE FSTA
 5 FILE GENBANK
 1 FILE IFIPAT
 0* FILE KOSMET
 0* FILE NTIS
 0* FILE NUTRACEUT
 1* FILE PASCAL
 0* FILE PHARMAML
 1 FILE SCISEARCH
 1 FILE TOXCENTER
 60 FILES SEARCHED...
 21 FILE USPATFULL
 3 FILE USPAT2
 0* FILE WATER
 2 FILE WPIDS
 2 FILE WPINDEX

13 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L1 QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?

=> file biotechds biotechabs caplus frosti genbank ifipat pascal scisearch
 toxcenter uspatfull uspat2

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	3.90	4.11

FILE 'BIOTECHDS' ENTERED AT 13:59:37 ON 07 JUL 2008
 COPYRIGHT (C) 2008 THOMSON REUTERS

FILE 'BIOTECHABS' ACCESS NOT AUTHORIZED

FILE 'CAPLUS' ENTERED AT 13:59:37 ON 07 JUL 2008
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 PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
 COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'FROSTI' ENTERED AT 13:59:37 ON 07 JUL 2008
 COPYRIGHT (C) 2008 Leatherhead Food Research Association

FILE 'GENBANK' ENTERED AT 13:59:37 ON 07 JUL 2008

FILE 'IFIPAT' ENTERED AT 13:59:37 ON 07 JUL 2008
 COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

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FILE 'SCISEARCH' ENTERED AT 13:59:37 ON 07 JUL 2008
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FILE 'TOXCENTER' ENTERED AT 13:59:37 ON 07 JUL 2008
 COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPATFULL' ENTERED AT 13:59:37 ON 07 JUL 2008
 CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 13:59:37 ON 07 JUL 2008
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

```
=> s l1
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
L2          38 L1
```

```
=> rem dup l2
DUP IS NOT VALID HERE
The DELETE command is used to remove various items stored by the
system.
```

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:

```
DELETE BIO?/Q          - delete query names starting with BIO
DELETE ?DRUG/A         - delete answer set names ending with DRUG
DELETE ?ELEC?/L        - delete L-number lists containing ELEC
DELETE ANTICOAG/S      - delete SDI request
DELETE ENZYME/B        - delete batch request
DELETE .MYCLUSTER      - delete user-defined cluster
DELETE .MYFORMAT       - delete user-defined display format
DELETE .MYFIELD        - delete user-defined search field
DELETE NAMELIST MYLIST - delete mailing list
```

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C        - delete print request
DELETE D134002C        - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21             - delete a single L-number
DELETE L3-L6           - delete a range of L-numbers
DELETE LAST 4          - delete the last 4 L-numbers
DELETE L33-            - delete L33 and any higher L-number
DELETE -L55            - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER  - delete a range of L-numbers and
                        renumber remaining L-numbers
DELETE RENUMBER        - renumber L-numbers after deletion of
                        intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED - delete all saved queries, answer sets,
                and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT - delete all user-defined display formats
DELETE FIELD - delete all user-defined search fields
DELETE SELECT - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l2
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L2
L3          34 DUP REM L2 (4 DUPLICATES REMOVED)
```

```
=> s l3 and (tablet or food or dietary supplement or confectionery or drug) and
product
L4          27 L3 AND (TABLET OR FOOD OR DIETARY SUPPLEMENT OR CONFECTIONERY
                OR DRUG) AND PRODUCT
```

```
=> rem dup l4
DUP IS NOT VALID HERE
The DELETE command is used to remove various items stored by the
system.
```

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:

```
DELETE BIO?/Q - delete query names starting with BIO
DELETE ?DRUG/A - delete answer set names ending with DRUG
DELETE ?ELEC?/L - delete L-number lists containing ELEC
DELETE ANTICOAG/S - delete SDI request
DELETE ENZYME/B - delete batch request
DELETE .MYCLUSTER - delete user-defined cluster
DELETE .MYFORMAT - delete user-defined display format
DELETE .MYFIELD - delete user-defined search field
DELETE NAMELIST MYLIST - delete mailing list
```

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C - delete print request
DELETE D134002C - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21           - delete a single L-number
DELETE L3-L6         - delete a range of L-numbers
DELETE LAST 4        - delete the last 4 L-numbers
DELETE L33-          - delete L33 and any higher L-number
DELETE -L55          - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                      renumber remaining L-numbers
DELETE RENUMBER      - renumber L-numbers after deletion of
                      intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED   - delete all saved queries, answer sets,
                  and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT  - delete all user-defined display formats
DELETE FIELD   - delete all user-defined search fields
DELETE SELECT  - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                  session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l4
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L4
L5          27 DUP REM L4 (0 DUPLICATES REMOVED)
```

```
=> d 15 1-27
```

```
L5  ANSWER 1 OF 27  USPATFULL on STN
AN   2007:296111  USPATFULL
TI   Lactobacillus acidophillus nucleic acid sequences encoding cell surface
      protein homologues and uses therefore
IN   Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
      Altermann, Eric, Palmerston North, NEW ZEALAND
      Buck, B. Logan, Banner Elk, NC, UNITED STATES
      Russell, W. Michael, Newburgh, IN, UNITED STATES
PA   North Carolina State University, Raleigh, NC, UNITED STATES (U.S.
      corporation)
PI   US 20070258955      A1  20071108
AI   US 2007-701335      A1  20070201 (11)
RLI  Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING
```

PRAI US 2003-465621P 20030425 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5104
 INCL INCLM: 424/093.400
 INCLS: 435/252.100; 435/252.900; 435/320.100; 435/006.000; 435/007.100;
 435/070.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100
 NCL NCLM: 424/093.400
 NCLS: 435/006.000; 435/007.100; 435/070.100; 435/252.100; 435/252.900;
 435/320.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100
 IC IPCI A61K0035-00 [I,A]; A61K0038-00 [I,A]; A61P0001-00 [I,A];
 C07H0021-02 [I,A]; C07H0021-00 [I,C*]; C07K0016-00 [I,A];
 C07K0004-00 [I,A]; C12N0001-20 [I,A]; C12N0015-00 [I,A];
 C12P0021-04 [I,A]; C12Q0001-68 [I,A]
 IPCR A61K0035-00 [I,C]; A61K0035-00 [I,A]; A61K0038-00 [I,C];
 A61K0038-00 [I,A]; A61P0001-00 [I,C]; A61P0001-00 [I,A];
 C07H0021-00 [I,C]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0004-00 [I,C]; C07K0004-00 [I,A]; C07K0014-195 [I,C*];
 C07K0014-335 [I,A]; C07K0016-00 [I,C]; C07K0016-00 [I,A];
 C12N0001-20 [I,C]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
 C12N0015-00 [I,C]; C12N0015-00 [I,A]; C12P0021-04 [I,C];
 C12P0021-04 [I,A]; C12P0021-06 [I,C*]; C12P0021-06 [I,A];
 C12Q0001-68 [I,C]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 2 OF 27 USPATFULL on STN
 AN 2007:197155 USPATFULL
 TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface
 protein homologues and uses therefore
 IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
 Altermann, Eric, Palmerston North, NEW ZEALAND
 Buck, B. Logan, Banner Elk, NC, UNITED STATES
 Russell, W. Michael, Newburgh, IN, UNITED STATES
 PA North Carolina State University, Raleigh, NC, UNITED STATES, 27695-8210
 (U.S. corporation)
 PI US 20070172495 A1 20070726
 AI US 2007-701319 A1 20070201 (11)
 RLI Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING
 PRAI US 2003-465621P 20030425 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5104
 INCL INCLM: 424/234.100
 INCLS: 514/044.000; 435/006.000; 435/007.320; 435/069.100; 435/252.900;
 435/471.000; 530/350.000; 536/023.700
 NCL NCLM: 424/234.100
 NCLS: 435/006.000; 435/007.320; 435/069.100; 435/252.900; 435/471.000;
 514/044.000; 530/350.000; 536/023.700
 IC IPCI A61K0048-00 [I,A]; A61K0039-02 [I,A]; C12Q0001-68 [I,A];
 G01N0033-554 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*];
 C12P0021-06 [I,A]; C07K0014-335 [I,A]; C07K0014-195 [I,C*]
 IPCR A61K0048-00 [I,C]; A61K0048-00 [I,A]; A61K0039-02 [I,C];
 A61K0039-02 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];
 C07K0014-195 [I,C]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
 C12P0021-06 [I,C]; C12P0021-06 [I,A]; C12Q0001-68 [I,C];
 C12Q0001-68 [I,A]; G01N0033-554 [I,C]; G01N0033-554 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 3 OF 27 USPATFULL on STN
 AN 2007:140436 USPATFULL

TI Delivery of trefoil peptides
IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
Steidler, Lothar, Lokeren, BELGIUM
Remaut, Erik Rene, Lovendegem, BELGIUM
PI US 20070122427 A1 20070531
AI US 2007-654879 A1 20070118 (11)
RLI Division of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A 371
of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000
PRAI EP 1999-870143 19990705
DT Utility
FS APPLICATION
LN.CNT 1335
INCL INCLM: 424/200.100
INCLS: 435/252.300; 435/252.900
NCL NCLM: 424/200.100
NCLS: 435/252.300; 435/252.900
IC IPCI A61K0039-02 [I,A]; C12N0001-21 [I,A]
IPCR A61K0039-02 [I,C]; A61K0039-02 [I,A]; C12N0001-21 [I,C];
C12N0001-21 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 4 OF 27 USPATFULL on STN
AN 2007:134502 USPATFULL
TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
(non-U.S. corporation)
PI US 20070117183 A1 20070524
AI US 2006-511140 A1 20060828 (11)
RLI Division of Ser. No. US 2005-55822, filed on 11 Feb 2005, PENDING
Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
PRAI DE 1999-19932125 19990709
DE 1999-19932227 19990709
DE 1999-19932228 19990709
DE 1999-19932230 19990709
DE 1999-19933005 19990714
DE 1999-19933006 19990714
DE 1999-19940764 19990827
DE 1999-19940766 19990827
DE 1999-19940832 19990827
DE 1999-19941378 19990831
DE 1999-19941379 19990831
DE 1999-19942077 19990903
DE 1999-19942079 19990903
DE 1999-19931418 19990708
DE 1999-19932126 19990709
DE 1999-19932229 19990709
DE 1999-19941396 19990831
DE 1999-19942087 19990903
DE 1999-19930476 19990701
DE 1999-19931419 19990708
DE 1999-19931420 19990708
DE 1999-19932206 19990709
DE 1999-19942088 19990903
DE 1999-19942124 19990903
DE 1999-19932928 19990714
DE 1999-19931415 19990708
DE 1999-19931424 19990708

DE	1999-19931428	19990708
DE	1999-19931434	19990708
DE	1999-19931435	19990708
DE	1999-19931443	19990708
DE	1999-19931453	19990708
DE	1999-19931457	19990708
DE	1999-19931465	19990708
DE	1999-19931478	19990708
DE	1999-19931510	19990708
DE	1999-19931541	19990708
DE	1999-19931573	19990708
DE	1999-19931592	19990708
DE	1999-19931632	19990708
DE	1999-19931634	19990708
DE	1999-19931636	19990708
DE	1999-19932130	19990709
DE	1999-19932186	19990709
DE	1999-19932922	19990714
DE	1999-19932926	19990714
DE	1999-19933004	19990714
DE	1999-19940765	19990827
DE	1999-19941380	19990831
DE	1999-19941394	19990831
DE	1999-19942076	19990903
DE	1999-19942086	19990903
DE	1999-19942095	19990903
DE	1999-19942129	19990903
US	1999-141031P	19990625 (60)
US	1999-142101P	19990702 (60)
US	1999-148613P	19990812 (60)
US	2000-187970P	20000309 (60)

DT Utility
FS APPLICATION

LN.CNT 8386

INCL INCL: 435/069.100
INCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
536/023.200

NCL NCLM: 435/069.100
NCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
536/023.200

IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12P0021-06 [I,A];
C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
C12N0009-10 [I,A]; C12N0015-74 [I,A]; C12N0001-21 [I,A]
IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C];
C12N0001-21 [I,A]; C12N0009-10 [I,C]; C12N0009-10 [I,A];
C12N0015-74 [I,C]; C12N0015-74 [I,A]; C12P0013-00 [I,C];
C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0021-06 [I,C];
C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 5 OF 27 USPATFULL on STN

AN 2007:127377 USPATFULL

TI Delivery of trefoil peptides

IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
Steidler, Lothar, Lokeren, BELGIUM
Remaut, Erik Rene, Lovendegem, BELGIUM

PI US 20070110723 A1 20070517

AI US 2007-654985 A1 20070118 (11)

RLI Continuation of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A
371 of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000

PRAI EP 1999-870143 19990705

DT Utility

FS APPLICATION
LN.CNT 1328
INCL INCLM: 424/093.200
INCLS: 424/093.450
NCL NCLM: 424/093.200
NCLS: 424/093.450
IC IPCI A61K0048-00 [I,A]
IPCR A61K0048-00 [I,C]; A61K0048-00 [I,A]; C12N0015-09 [I,C*];
C12N0015-09 [I,A]; A61K0035-66 [I,C*]; A61K0035-74 [I,A];
A61K0038-00 [I,C*]; A61K0038-00 [I,A]; A61P0001-00 [I,C*];
A61P0001-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-575 [I,A];
C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0015-16 [I,C*];
C12N0015-16 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
C12R0001-01 [N,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 6 OF 27 USPATFULL on STN
AN 2007:130427 USPATFULL
TI Delivery of trefoil peptides
IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
Steidler, Lothar, Lokeren, BELGIUM
Remaut, Erik Rene, Lonendegem, BELGIUM
PA Vlaams Interuniversitair Instituut voor Biotechnologie, BELGIUM
(non-U.S. corporation)
PI US 7220418 B1 20070522
WO 2001002570 20010111
AI US 2000-30390 20000705 (10)
WO 2000-EP6343 20000705
20020416 PCT 371 date
PRAI EP 1999-870143 19990705
DT Utility
FS GRANTED
LN.CNT 1334
INCL INCLM: 424/200.100
INCLS: 424/093.450; 424/093.200; 424/234.100; 424/192.100; 514/925.000
NCL NCLM: 424/200.100
NCLS: 424/093.200; 424/093.450; 424/192.100; 424/234.100; 514/925.000
IC IPCI A01N0063-00 [I,A]; A61K0039-02 [I,A]; A61K0039-00 [I,A]
IPCR A01N0063-00 [I,C]; A01N0063-00 [I,A]; C12N0015-09 [I,C*];
C12N0015-09 [I,A]; A61K0035-66 [I,C*]; A61K0035-74 [I,A];
A61K0038-00 [I,C*]; A61K0038-00 [I,A]; A61K0039-00 [I,C];
A61K0039-00 [I,A]; A61K0039-02 [I,C]; A61K0039-02 [I,A];
A61K0048-00 [I,C*]; A61K0048-00 [I,A]; A61P0001-00 [I,C*];
A61P0001-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-575 [I,A];
C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0015-16 [I,C*];
C12N0015-16 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
C12R0001-01 [N,A]
EXF 424/200.1; 424/192.1; 424/184.1; 424/234.1; 424/244.1; 424/246.1;
424/93.2; 424/93.45; 514/2; 514/925; 435/69.3; 435/69.1; 435/71.1;
435/252.9
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 7 OF 27 IFIPAT COPYRIGHT 2008 IFI on STN
AN 11053905 IFIPAT;IFIUDB;IFICDB
TI METHOD OF IMPROVING IMMUNE FUNCTION IN MAMALS USING LACTOBACILLUS
REUTERI STRAINS
IN Kang Ho-Jin (KR); Kwon Ik-boo (KR); Lee Dong-Seog (KR); Mollstam Bo (SE)
PA Unassigned Or Assigned To Individual (68000)
PI US 2006002907 A1 20060105
AI US 2002-531651 20021018
WO 2002-SE1903 20021018
20050415 PCT 371 date

20050415 PCT 102(e) date
FI US 2006002907 20060105
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
ED Entered STN: 9 Jan 2006
Last Updated on STN: 9 Jan 2006
CLMN 9
GI 1 Figure(s).
FIG. 1. Confirmation of inhibitory ability against the binding of vero
cytotoxin(VT) and Gb3 receptor in a culture supernatant of L. reuteri
through competitive ELISA. Each reacted as follows, on plates coated with
Gb3, followed by performing ELISA using mAb against VT.

L5 ANSWER 8 OF 27 USPATFULL on STN
AN 2006:274450 USPATFULL
TI Gene products differentially expressed in cancerous cells
IN Scott, Elizabeth M., Emeryville, CA, UNITED STATES
Lamson, George, Emeryville, CA, UNITED STATES
Kassam, Altaf, Emeryville, CA, UNITED STATES
Zhang, Guozhong, Emeryville, CA, UNITED STATES
Sakamoto, Doreen, Emeryville, CA, UNITED STATES
Garcia, Pablo Dominguez, Emeryville, CA, UNITED STATES
May, Theresa, Emeryville, CA, UNITED STATES
Kennedy, Giulia C., Emeryville, CA, UNITED STATES
Kang, Sanmao, Emeryville, CA, UNITED STATES
Reinhard, Christoph, Emeryville, CA, UNITED STATES
Jefferson, Ann Bennett, Emeryville, CA, UNITED STATES
PA Chiron Corporation (U.S. corporation)
PI US 20060234246 A1 20061019
AI US 2004-934842 A1 20040902 (10)
RLI Continuation-in-part of Ser. No. US 2002-165835, filed on 6 Jun 2002,
ABANDONED Continuation of Ser. No. US 2000-490818, filed on 25 Jan 2000,
GRANTED, Pat. No. US 6429302 Continuation-in-part of Ser. No. US
2001-883152, filed on 15 Jun 2001, ABANDONED Continuation-in-part of
Ser. No. WO 2003-US15465, filed on 16 May 2003, PENDING
PRAI US 1999-118302P 19990202 (60)
US 2000-211835P 20000615 (60)
US 2003-445222P 20030204 (60)
US 2002-381533P 20020517 (60)
DT Utility
FS APPLICATION
LN.CNT 17024
INCL INCLM: 435/006.000
INCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
530/388.800; 536/023.500
NCL NCLM: 435/006.000
NCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
530/388.800; 536/023.500
IC IPCI C12Q0001-68 [I,A]; G01N0033-574 [I,A]; C07H0021-04 [I,A];
C07H0021-00 [I,C*]; C12P0021-06 [I,A]; C07K0014-82 [I,A];
C07K0016-30 [I,A]; C07K0016-18 [I,C*]
IPCR C12Q0001-68 [I,C]; C12Q0001-68 [I,A]; C07H0021-00 [I,C];
C07H0021-04 [I,A]; C07K0014-82 [I,C]; C07K0014-82 [I,A];
C07K0016-18 [I,C]; C07K0016-30 [I,A]; C12P0021-06 [I,C];
C12P0021-06 [I,A]; G01N0033-574 [I,C]; G01N0033-574 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 9 OF 27 USPATFULL on STN
AN 2006:98984 USPATFULL
TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF

Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
 (non-U.S. corporation)
 PI US 20060084152 A1 20060420
 AI US 2005-239674 A1 20050928 (11)
 RLI Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED
 Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
 ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23
 Jun 2000, ABANDONED
 PRAI DE 1999-19932125 19990709
 DE 1999-19932227 19990709
 DE 1999-19932228 19990709
 DE 1999-19932230 19990709
 DE 1999-19933005 19990714
 DE 1999-19933006 19990714
 DE 1999-19940764 19990827
 DE 1999-19940766 19990827
 DE 1999-19940832 19990827
 DE 1999-19941378 19990831
 DE 1999-19941379 19990831
 DE 1999-19942077 19990903
 DE 1999-19942079 19990903
 DE 1999-19931418 19990708
 DE 1999-19932126 19990709
 DE 1999-19932229 19990709
 DE 1999-19941396 19990831
 DE 1999-19942087 19990903
 DE 1999-19930476 19990701
 DE 1999-19931419 19990708
 DE 1999-19931420 19990708
 DE 1999-19932206 19990709
 DE 1999-19942088 19990903
 DE 1999-19942124 19990903
 DE 1999-19932928 19990714
 DE 1999-19931415 19990708
 DE 1999-19931424 19990708
 DE 1999-19931428 19990708
 DE 1999-19931434 19990708
 DE 1999-19931435 19990708
 DE 1999-19931443 19990708
 DE 1999-19931453 19990708
 DE 1999-19931457 19990708
 DE 1999-19931465 19990708
 DE 1999-19931478 19990708
 DE 1999-19931510 19990708
 DE 1999-19931541 19990708
 DE 1999-19931573 19990708
 DE 1999-19931592 19990708
 DE 1999-19931632 19990708
 DE 1999-19931634 19990708
 DE 1999-19931636 19990708
 DE 1999-19932130 19990708
 DE 1999-19932186 19990709
 DE 1999-19932922 19990714
 DE 1999-19932926 19990714
 DE 1999-19933004 19990714
 DE 1999-19940765 19990827
 DE 1999-19941380 19990831
 DE 1999-19941394 19990831

DE 1999-19942076 19990903
 DE 1999-19942086 19990903
 DE 1999-19942095 19990903
 DE 1999-19942129 19990903
 DE 1999-19932124 19990709
 DE 1999-19932127 19990709
 DE 1999-19932133 19990709
 DE 1999-19932207 19990709
 DE 1999-19932208 19990709
 DE 1999-19932225 19990709
 DE 1999-19932914 19990709
 DE 1999-19940768 19990827
 DE 1999-19940831 19990827
 DE 1999-19941385 19990831
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)
 US 1999-141031P 19990625 (60)
 US 1999-143694P 19990714 (60)
 US 1999-151778P 19990831 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 14822
 INCL INCLM: 435/113.000
 INCLS: 435/115.000; 435/252.300
 NCL NCLM: 435/113.000
 NCLS: 435/115.000; 435/252.300
 IC IPCI C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
 C12N0001-20 [I,A]
 IPCR C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];
 C12N0001-20 [I,A]; C12P0013-08 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

 L5 ANSWER 10 OF 27 USPATFULL on STN
 AN 2006:211028 USPATFULL
 TI Nucleic acid sequences relating to Bacteroides fragilis for diagnostics
 and therapeutics
 IN Breton, Gary L., Marlboro, MA, UNITED STATES
 PA Oscient Pharmaceuticals Corporation, Waltham, MA, UNITED STATES (U.S.
 corporation)
 PI US 7090973 B1 20060815
 AI US 2000-540209 20000404 (9)
 PRAI US 1999-128705P 19990409 (60)
 DT Utility
 FS GRANTED
 LN.CNT 38850
 INCL INCLM: 435/006.000
 INCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
 NCL NCLM: 435/006.000
 NCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
 IC IPCI C12Q0001-68 [I,A]; C12P0019-34 [I,A]; C12P0019-00 [I,C*];
 C07H0021-02 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*]
 EXF 435/91.1; 435/91.2; 435/6; 435/320.1; 435/325; 435/352.3; 536/23.1;
 536/24.1; 536/23.7; 536/24.32; 536/24.3; 514/44
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

 L5 ANSWER 11 OF 27 USPATFULL on STN
 AN 2006:146715 USPATFULL
 TI Nucleic acid and amino acid sequences relating to Staphylococcus
 epidermidis for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn, Framingham, MA, UNITED STATES

Bush, David, Somerville, MA, UNITED STATES
 PA Wyeth, Madison, NJ, UNITED STATES (U.S. corporation)
 PI US 7060458 B1 20060613
 AI US 1999-450969 19991129 (9)
 RLI Continuation-in-part of Ser. No. US 1998-134001, filed on 13 Aug 1998,
 Pat. No. US 6380370, issued on 30 Apr 2002
 PRAI US 1997-64964P 19971108 (60)
 US 1997-55779P 19970814 (60)
 DT Utility
 FS GRANTED
 LN.CNT 35708
 INCL INCLM: 435/069.100
 INCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
 NCL NCLM: 435/069.100
 NCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
 IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C*]
 IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]
 EXF 435/6; 435/91.2; 435/69.1; 536/22.1; 536/23.1; 536/24.3
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 12 OF 27 USPATFULL on STN
 AN 2005:299042 USPATFULL
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
 (non-U.S. corporation)
 PI US 20050260707 A1 20051124
 AI US 2005-55822 A1 20050211 (11)
 RLI Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
 PRAI DE 1999-19932125 19990709
 DE 1999-19932227 19990709
 DE 1999-19932228 19990709
 DE 1999-19932230 19990709
 DE 1999-19933005 19990714
 DE 1999-19933006 19990714
 DE 1999-19940764 19990827
 DE 1999-19940766 19990827
 DE 1999-19940832 19990827
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 DE 1999-19942077 19990903
 DE 1999-19942079 19990903
 DE 1999-19931418 19990708
 DE 1999-19932126 19990709
 DE 1999-19932229 19990709
 DE 1999-19941396 19990831
 DE 1999-19942087 19990903
 DE 1999-19930476 19990701
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 DE 1999-19932206 19990709
 DE 1999-19942088 19990903
 DE 1999-19942124 19990903
 DE 1999-19932928 19990714
 DE 1999-19931415 19990708
 DE 1999-19931424 19990708
 DE 1999-19931428 19990708

DE	1999-19931434	19990708
DE	1999-19931435	19990708
DE	1999-19931443	19990708
DE	1999-19931453	19990708
DE	1999-19931457	19990708
DE	1999-19931465	19990708
DE	1999-19931478	19990708
DE	1999-19931510	19990708
DE	1999-109931541	19990708
DE	1999-19931573	19990708
DE	1999-19931592	19990708
DE	1999-19931632	19990708
DE	1999-19931634	19990708
DE	1999-19931636	19990708
DE	1999-19932130	19990708
DE	1999-19932186	19990709
DE	1999-19932922	19990714
DE	1999-19932926	19990714
DE	1999-19933004	19990714
DE	1999-19940765	19990827
DE	1999-19941380	19990831
DE	1999-19941394	19990831
DE	1999-19942076	19990903
DE	1999-19942086	19990903
DE	1999-19942095	19990903
DE	1999-19942129	19990903
US	1999-141031P	19990625 (60)
US	1999-142101P	19990702 (60)
US	1999-148613P	19990812 (60)
US	2000-187970P	20000309 (60)

DT Utility

FS APPLICATION

LN.CNT 8777

INCL INCLM: 435/069.100

INCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200

NCL NCLM: 435/069.100

NCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200

IC [7]

ICM C12P021-06

ICS C12P013-04; C07H021-04; C12N001-20; C12N015-74; C12N009-10

IPCI C12P0021-06 [ICM,7]; C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*];
C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]; C12N0001-20 [ICS,7];
C12N0015-74 [ICS,7]; C12N0009-10 [ICS,7]

IPCR C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
C07K0014-34 [I,A]; C12N0001-20 [I,C*]; C12N0001-20 [I,A];
C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
C12P0013-00 [I,C*]; C12P0013-04 [I,A]; C12P0021-06 [I,C*];
C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 13 OF 27 USPATFULL on STN

AN 2005:268092 USPATFULL

TI Modified bacterial surface layer proteins

IN Pouwels, Pieter Hendrik, Rijswijk, NETHERLANDS

Smit, Egbert, Sittard, NETHERLANDS

Tielen, Frans, Prinsenbeek, NETHERLANDS

PI US 20050233408 A1 20051020

AI US 2003-500307 A1 20021223 (10)

WO 2002-EP14749 20021223

20041122 PCT 371 date

PRAI EP 2001-310937 20011228

DT Utility
 FS APPLICATION
 LN.CNT 2664
 INCL INCLM: 435/034.000
 INCLS: 530/395.000; 435/252.300
 NCL NCLM: 435/034.000
 NCLS: 435/252.300; 530/395.000
 IC [7]
 ICM C12Q001-04
 ICS C12N001-21; C07K014-335
 IPCI C12Q0001-04 [ICM,7]; C12N0001-21 [ICS,7]; C07K0014-335 [ICS,7];
 C07K0014-195 [ICS,7,C*]
 IPCR C12N0015-09 [I,C*]; C12N0015-09 [I,A]; A61K0039-02 [I,C*];
 A61K0039-02 [I,A]; A61P0031-00 [I,C*]; A61P0031-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-15 [I,C*];
 C12N0001-15 [I,A]; C12N0001-19 [I,C*]; C12N0001-19 [I,A];
 C12N0001-20 [I,C*]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0005-10 [I,C*]; C12N0005-10 [I,A];
 C12N0015-31 [I,C*]; C12N0015-31 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 14 OF 27 USPATFULL on STN
 AN 2005:220997 USPATFULL
 TI Corynebacterium glutamicum genes encoding proteins involved in
 homeostasis and adaptation
 IN Pompejus, Markus, Waldsee, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 PA Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF,
 D-67056 (non-U.S. corporation)
 PI US 20050191732 A1 20050901
 AI US 2003-721922 A1 20031124 (10)
 RLI Continuation of Ser. No. US 2000-603124, filed on 23 Jun 2000, ABANDONED
 PRAI DE 1999-19931418 19990708
 DE 1999-19932124 19990709
 DE 1999-19932126 19990709
 DE 1999-19932127 19990709
 DE 1999-19932133 19990709
 DE 1999-19932207 19990709
 DE 1999-19932208 19990709
 DE 1999-19932225 19990709
 DE 1999-19932229 19990709
 DE 1999-19932914 19990709
 DE 1999-19933006 19990709
 DE 1999-19940765 19990827
 DE 1999-19940768 19990827
 DE 1999-19940831 19990827
 DE 1999-19940832 19990827
 DE 1999-19941385 19990831
 DE 1999-19941396 19990831
 DE 1999-19942087 19990903
 US 1999-141031P 19990625 (60)
 US 1999-143694P 19990714 (60)
 US 1999-151778P 19990831 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 6552
 INCL INCLM: 435/106.000
 INCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
 536/023.200

NCL NCLM: 435/106.000
 NCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
 536/023.200

IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12P013-04; C12N009-10; C12N001-21; C12N015-74
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*]; C12N0009-10 [ICS,7];
 C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7]
 IPCR C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
 C07K0014-34 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
 C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
 C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
 C12P0001-04 [I,C*]; C12P0001-04 [I,A]; C12P0013-00 [I,C*];
 C12P0013-04 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 15 OF 27 USPATFULL on STN
 AN 2005:158196 USPATFULL
 TI Nucleic acid and amino acid sequences relating to streptococcus
 pneumoniae for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn A., Framingham, MA, UNITED STATES
 Bush, David, Somerville, MA, UNITED STATES
 PI US 20050136404 A1 20050623
 AI US 2003-617320 A1 20030710 (10)
 RLI Division of Ser. No. US 1998-107433, filed on 30 Jun 1998, PENDING
 PRAI US 1997-51553P 19970702 (60)
 US 1998-85131P 19980512 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 12957
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
 NCL NCLM: 435/006.000
 NCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
 IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12N001-21; C07K014-315
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12N0001-21 [ICS,7]; C07K0014-315 [ICS,7]; C07K0014-195
 [ICS,7,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-315 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 16 OF 27 USPATFULL on STN
 AN 2005:131152 USPATFULL
 TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface
 protein homologues and uses therefore
 IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
 Alterman, Eric, Apex, NC, UNITED STATES
 Buck, B. Logan, Banner Elk, NC, UNITED STATES
 Russell, W. Michael, Newburg, IN, UNITED STATES
 PI US 20050112612 A1 20050526
 US 7348420 B2 20080325
 AI US 2004-831070 A1 20040423 (10)
 PRAI US 2003-465621P 20030425 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 6100
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 530/350.000;

536/023.200
NCL NCLM: 536/023.100; 435/006.000
NCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 530/350.000;
536/023.200
IC [7]
ICM C12Q001-68
ICS C07H021-04; C12P021-06; C12N009-00; C12N001-21; C07K014-335
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
C12P0021-06 [ICS,7]; C12N0009-00 [ICS,7]; C12N0001-21 [ICS,7];
C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
IPCI-2 C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12N0001-20 [I,A];
C12N0015-00 [I,A]; C12P0001-20 [I,A]
IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
C07K0014-335 [I,A]; C12N0001-20 [I,C]; C12N0001-20 [I,A];
C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0009-00 [I,C*];
C12N0009-00 [I,A]; C12N0015-00 [I,C]; C12N0015-00 [I,A];
C12P0021-06 [I,C*]; C12P0021-06 [I,A]; C12Q0001-68 [I,C*];
C12Q0001-68 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 27 USPATFULL on STN
AN 2004:95339 USPATFULL
TI Nutritional formulations containing synbiotic substances
IN Kaup, Susan M., Collingswood, NJ, UNITED STATES
Wilson, Jeffrey L., Doylestown, PA, UNITED STATES
Kostek, Beverley M., Glen Mills, PA, UNITED STATES
Frantz, David C., Pottstown, PA, UNITED STATES
PA Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)
PI US 20040072794 A1 20040415
AI US 2003-681658 A1 20031008 (10)
PRAI US 2002-418109P 20021011 (60)
DT Utility
FS APPLICATION
LN.CNT 542
INCL INCLM: 514/054.000
INCLS: 424/093.450
NCL NCLM: 514/054.000
NCLS: 424/093.450
IC [7]
ICM A61K045-00
ICS A61K031-715
IPCI A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]
IPCR A23L0001-052 [I,C*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C*];
A23L0001-29 [I,A]; A23L0001-30 [I,C*]; A23L0001-30 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 18 OF 27 USPATFULL on STN
AN 2004:12970 USPATFULL
TI Polynucleotides, materials incorporating them, and methods for using
them
IN Glenn, Matthew, Whenuapai, NEW ZEALAND
Havukkala, Ilkka J., Remuera, NEW ZEALAND
Lubbers, Mark, Palmerston North, NEW ZEALAND
Dekker, James, Palmerston North, NEW ZEALAND
PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND
(non-U.S. corporation)
PI US 20040009490 A1 20040115
US 7125698 B2 20061024
AI US 2002-264213 A1 20021003 (10)
RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,
PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug
2000, GRANTED, Pat. No. US 6544772

PRAI US 1999-147853P 19990809 (60)
 US 1999-147852P 19990809 (60)
 US 1999-152032P 19990901 (60)
 US 1999-152031P 19990901 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5375
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200
 NCL NCLM: 435/193.000; 435/006.000
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;
 435/252.300; 435/320.100; 536/023.200
 IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
 IPCI-2 C12N0009-10 [I,A]
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C*];
 A23C0019-032 [I,A]; A61K0038-00 [N,C*]; A61K0038-00 [N,A];
 C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 19 OF 27 USPATFULL on STN
 AN 2004:250212 USPATFULL
 TI Nucleic acid and amino acid sequences relating to Streptococcus
 pneumoniae for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn A., Framingham, MA, United States
 Bush, David, Somerville, MA, United States
 PA Genome Therapeutics Corporation, Waltham, MA, United States (U.S.
 corporation)
 PI US 6800744 B1 20041005
 AI US 1998-107433 19980630 (9)
 PRAI US 1998-85131P 19980512 (60)
 US 1997-51553P 19970702 (60)
 DT Utility
 FS GRANTED
 LN.CNT 11545
 INCL INCLM: 536/023.100
 INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;
 536/024.100; 536/023.400; 536/024.320
 NCL NCLM: 536/023.100
 NCLS: 435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;
 536/024.100; 536/024.320
 IC [7]
 ICM C12Q001-68
 ICS C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;
 C07H021-04
 IPCI C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];
 C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-315 [I,A]
 EXF 536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;
 435/6
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 20 OF 27 USPATFULL on STN
 AN 2003:71519 USPATFULL
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF

PI US 20030049804 A1 20030313
AI US 2000-746660 A1 20001222 (9)

RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
2000, PENDING

PRAI DE 1999-19931420 19990708
US 1999-141031P 19990625 (60)
US 1999-142101P 19990702 (60)
US 1999-148613P 19990812 (60)
US 2000-187970P 20000309 (60)

DT Utility
FS APPLICATION

LN.CNT 15004

INCL INCLM: 435/115.000
INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200

NCL NCLM: 435/115.000
NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200

IC [7]
ICM C12P013-08
ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21
IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
C12N0001-21 [ICS,7]
IPCR C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
C12N0009-90 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 21 OF 27 USPATFULL on STN

AN 2003:95966 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using
them

IN Glenn, Matthew, Auckland, NEW ZEALAND
Havukkala, Ilkka J., Auckland, NEW ZEALAND
Blokberg, Leonard N., Auckland, NEW ZEALAND
Lubbers, Mark W., Palmerston North, NEW ZEALAND
Dekker, James, Palmerston North, NEW ZEALAND
Christensson, Anna C., Lund, SWEDEN
Holland, Ross, Palmerston North, NEW ZEALAND
O'Toole, Paul W., Palmerston North, NEW ZEALAND
Reid, Julian R., Palmerston North, NEW ZEALAND
Coolbear, Timothy, Palmerston North, NEW ZEALAND

PA Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.
corporation)
Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.
corporation)

PI US 6544772 B1 20030408
AI US 2000-634238 20000808 (9)

DT Utility
FS GRANTED

LN.CNT 2015

INCL INCLM: 435/252.300
INCLS: 435/320.100; 536/023.700

NCL NCLM: 435/252.300
NCLS: 435/320.100; 536/023.700
IC [7]
ICM C12N001-21
ICS C12N015-63; C12N015-31
IPCI C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]
IPCR A23C0019-00 [I,C*]; A23C0019-032 [I,A]; C07K0014-195 [I,C*];
C07K0014-335 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
C12N0015-31 [I,C*]; C12N0015-31 [I,A]
EXF 435/252.3; 435/320.1; 536/23.7
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN
AN 1999-00562 BIOTECHDS
TI Use of lactic and propionic acid bacteria;
to bind mycotoxin to prevent their absorption or to purify
contaminated food or feedstuff
AU El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J
PA Roy.Melbourne-Inst.Technol.
LO Melbourne, Victoria, Australia.
PI WO 9834503 13 Aug 1998
AI WO 1998-AU63 6 Feb 1998
PRAI AU 1997-5005 7 Feb 1997
DT Patent
LA English
OS WPI: 1998-557001 [49]

L5 ANSWER 23 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): CP000705 GenBank (R)
GenBank ACC. NO. (GBN): CP000705 AAOV01000000 AAOV01000001-AAOV01000097
GenBank VERSION (VER): CP000705.1 GI:148530277
SEQUENCE LENGTH (SQL): 1999618
MOLECULE TYPE (CI): DNA; circular
DIVISION CODE (CI): Bacteria
DATE (DATE): 17 Oct 2007
DEFINITION (DEF): Lactobacillus reuteri F275,
complete genome.
SOURCE: Lactobacillus reuteri F275
ORGANISM (ORGN): Lactobacillus reuteri F275
Bacteria; Firmicutes; Lactobacillales;
Lactobacillaceae; Lactobacillus
PROJECT (PJID): GenomeProject:15766
COMMENT:

URL -- <http://www.jgi.doe.gov>
JGI Project ID: 4000135
Source DNA available from Gerald Tannock
(gerald.tannock@stonebow.otago.ac.nz)
Bacteria available from DSMZ: DSM 20016
Contacts: Gerald Tannock (gerald.tannock@stonebow.otago.ac.nz)
Paul Richardson (microbes@cuba.jgi-psf.org)
Quality assurance done by JGI-Stanford
Annotation done by JGI-ORNL and JGI-PGF
Finishing done by JGI-PGF
Finished microbial genomes have been curated to close all gaps with
greater than 98% coverage of at least two independent clones. Each
base pair has a minimum q (quality) value of 30 and the total error
rate is less than one per 50000.
The JGI and collaborators endorse the principles for the
distribution and use of large scale sequencing data adopted by the
larger genome sequencing community and urge users of this data to
follow them. It is our intention to publish the work of this

project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>).

REFERENCE: 1 (bases 1 to 1999618)
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
TITLE (TI): Complete sequence of chromosome of
Lactobacillus reuteri DSM 20016
JOURNAL (SO): Unpublished
REFERENCE: 2 (bases 1 to 1999618)
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (17-MAY-2007) US DOE Joint Genome Institute,
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,
USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1999618	/organism="Lactobacillus reuteri F275" /mol-type="genomic DNA" /strain="DSM 20016" /db-xref="taxon:299033" /note="F275 = DSM 20016 = JCM 1112"

L5 ANSWER 24 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM270397 GenBank (R)
GenBank ACC. NO. (GBN): AM270397
GenBank VERSION (VER): AM270397.1 GI:134084136
CAS REGISTRY NO. (RN): 928607-03-8
SEQUENCE LENGTH (SQL): 163680
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Plants, fungi, algae
DATE (DATE): 24 Mar 2007
DEFINITION (DEF): Aspergillus niger contig An18c0040, complete genome.
SOURCE: Aspergillus niger
ORGANISM (ORGN): Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic
Trichocomaceae; Aspergillus
REFERENCE: 1 (bases 150631 to 153085)
AUTHOR (AU): Habison,A.; Kubicek,C.P.; Rohr,M.
TITLE (TI): Partial purification and regulatory properties of
phosphofructokinase from Aspergillus niger
JOURNAL (SO): Biochem. J., 209 (3), 669-676 (1983)
OTHER SOURCE (OS): CA 99:171737
REFERENCE: 2 (bases 71863 to 73356)
AUTHOR (AU): Manney,T.R.
TITLE (TI): Expression of the BAR1 gene in Saccharomyces
cerevisiae: induction by the alpha mating pheromone of
an activity associated with a secreted protein

JOURNAL (SO): J. Bacteriol., 155 (1), 291-301 (1983)
 OTHER SOURCE (OS): CA 99:102121
 REFERENCE: 3 (bases 71863 to 73356)
 AUTHOR (AU): Jones, E.W.
 TITLE (TI): The synthesis and function of proteases in
 Saccharomyces: genetic approaches
 JOURNAL (SO): Annu. Rev. Genet., 18, 233-270 (1984)
 OTHER SOURCE (OS): CA 102:92538
 REFERENCE: 4 (bases 144032 to 145578)
 AUTHOR (AU): Brandsch, R.; Bichler, V.
 TITLE (TI): In vivo and in vitro expression of the
 6-hydroxy-D-nicotine oxidase gene of Arthrobacter
 oxidans, cloned into Escherichia coli, as an
 enzymatically active, covalently flavinylated
 polypeptide
 JOURNAL (SO): FEBS Lett., 192 (2), 204-208 (1985)
 OTHER SOURCE (OS): CA 104:29597
 REFERENCE: 5 (bases 150631 to 153085)
 AUTHOR (AU): Schrefler, G.; Kubicek, C.P.; Rohr, M.
 TITLE (TI): Inhibition of citric acid accumulation by manganese
 ions in Aspergillus niger mutants with reduced citrate
 control of phosphofructokinase
 JOURNAL (SO): J. Bacteriol., 165 (3), 1019-1022 (1986)
 OTHER SOURCE (OS): CA 104:165023
 REFERENCE: 6 (bases 156827 to 158638)
 AUTHOR (AU): Whittington, H.A.; Grant, S.; Roberts, C.F.; Lamb, H.;
 Hawkins, A.R.
 TITLE (TI): Identification and isolation of a putative permease
 gene in the quinic acid utilization (QUT) gene cluster
 of Aspergillus nidulans
 JOURNAL (SO): Curr. Genet., 12 (2), 135-139 (1987)
 OTHER SOURCE (OS): CA 107:91128
 REFERENCE: 7 (bases 54105 to 55762)
 AUTHOR (AU): Chisholm, V.T.; Lea, H.Z.; Rai, R.; Cooper, T.G.
 TITLE (TI): Regulation of allantate transport in wild-type and
 mutant strains of Saccharomyces cerevisiae
 JOURNAL (SO): J. Bacteriol., 169 (4), 1684-1690 (1987)
 OTHER SOURCE (OS): CA 106:172689
 REFERENCE: 8 (bases 71863 to 73356)
 AUTHOR (AU): MacKay, V.L.; Welch, S.K.; Insley, M.Y.; Manney, T.R.;
 Holly, J.; Saari, G.C.; Parker, M.L.
 TITLE (TI): The Saccharomyces cerevisiae BAR1 gene encodes an
 exported protein with homology to pepsin
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 85 (1), 55-59 (1988)
 OTHER SOURCE (OS): CA 108:125658
 REFERENCE: 9 (bases 54105 to 55762)
 AUTHOR (AU): Rai, R.; Genbauffe, F.S.; Cooper, T.G.
 TITLE (TI): Structure and transcription of the allantate permease
 gene (DAL5) from Saccharomyces cerevisiae
 JOURNAL (SO): J. Bacteriol., 170 (1), 266-271 (1988)
 OTHER SOURCE (OS): CA 109:17930
 REFERENCE: 10
 AUTHOR (AU): Hawkins, A.R.; Lamb, H.K.; Smith, M.; Keyte, J.W.;
 Roberts, C.F.
 TITLE (TI): Molecular organisation of the quinic acid utilization
 (QUT) gene cluster in Aspergillus nidulans
 JOURNAL (SO): Mol. Gen. Genet., 214 (2), 224-231 (1988)
 OTHER SOURCE (OS): CA 111:188522
 REFERENCE: 11 (bases 68231 to 69040)
 AUTHOR (AU): Honjo, M.; Nakayama, A.; Fukazawa, K.; Kawamura, K.;
 Ando, K.; Furutani, Y.
 TITLE (TI): A novel Bacillus subtilis gene involved in negative

control of sporulation and degradative-enzyme
production

JOURNAL (SO): J. Bacteriol., 172 (4), 1783-1790 (1990)
OTHER SOURCE (OS): CA 113:146166
REFERENCE: 12 (bases 5212 to 7379)
AUTHOR (AU): Nikawa,J.; Hosaka,K.; Tsukagoshi,Y.; Yamashita,S.
TITLE (TI): Primary structure of the yeast choline transport gene
and regulation of its expression

JOURNAL (SO): J. Biol. Chem., 265 (26), 15996-16003 (1990)
OTHER SOURCE (OS): CA 114:18549
REFERENCE: 13 (bases 159975 to 161849)
AUTHOR (AU): Fling,M.E.; Kopf,J.; Tamarkin,A.; Gorman,J.A.;
Smith,H.A.; Koltin,Y.
TITLE (TI): Analysis of a Candida albicans gene that encodes a
novel mechanism for resistance to benomyl and
methotrexate

JOURNAL (SO): Mol. Gen. Genet., 227 (2), 318-329 (1991)
OTHER SOURCE (OS): CA 116:100405
REFERENCE: 14 (bases 28874 to 30837)
AUTHOR (AU): Masuda,N.; Kitamura,N.; Saito,K.
TITLE (TI): Primary structure of protein moiety of Penicillium
notatum phospholipase B deduced from the cDNA

JOURNAL (SO): Eur. J. Biochem., 202 (3), 783-787 (1991)
OTHER SOURCE (OS): CA 118:76020
REFERENCE: 15 (bases 100363 to 101496)
AUTHOR (AU): Sakoda,H.; Imanaka,T.
TITLE (TI): Cloning and sequencing of the gene coding for alcohol
dehydrogenase of Bacillus stearothermophilus and
rational shift of the optimum pH

JOURNAL (SO): J. Bacteriol., 174 (4), 1397-1402 (1992)
OTHER SOURCE (OS): CA 118:186708
REFERENCE: 16 (bases 20773 to 22555)
AUTHOR (AU): Kamoda,S.; Saburi,Y.
TITLE (TI): Structural and enzymatical comparison of
lignostilbene-alpha,beta-dioxygenase isozymes, I, II,
and III, from Pseudomonas paucimobilis TMY1009

JOURNAL (SO): Biosci. Biotechnol. Biochem., 57 (6), 931-934 (1993)
OTHER SOURCE (OS): CA 119:154577
REFERENCE: 17 (bases 80602 to 83154)
AUTHOR (AU): ElBerry,H.M.; Majumdar,M.L.; Cunningham,T.S.;
Sumrada,R.A.; Cooper,T.G.
TITLE (TI): Regulation of the urea active transporter gene (DUR3)
in Saccharomyces cerevisiae

JOURNAL (SO): J. Bacteriol., 175 (15), 4688-4698 (1993)
OTHER SOURCE (OS): CA 119:242524
REFERENCE: 18 (bases 23096 to 24052)
AUTHOR (AU): Roper,D.I.; Cooper,R.A.
TITLE (TI): Purification, nucleotide sequence and some properties
of a bifunctional isomerase/decarboxylase from the
homoprotocatechuate degradative pathway of Escherichia
coli C

JOURNAL (SO): Eur. J. Biochem., 217 (2), 575-580 (1993)
OTHER SOURCE (OS): CA 119:265270
REFERENCE: 19 (bases 5212 to 7379)
AUTHOR (AU): Li,Z.; Brendel,M.
TITLE (TI): Co-regulation with genes of phospholipid biosynthesis
of the CTR/HNMI-encoded choline/nitrogen mustard
permease in Saccharomyces cerevisiae

JOURNAL (SO): Mol. Gen. Genet., 241 (5-6), 680-684 (1993)
OTHER SOURCE (OS): CA 121:28475
REFERENCE: 20 (bases 159975 to 161849)
AUTHOR (AU): Ben-Yaacov,R.; Knoller,S.; Caldwell,G.A.; Becker,J.M.;

Koltin, Y.

TITLE (TI): Candida albicans gene encoding resistance to benomyl and methotrexate is a multidrug resistance gene

JOURNAL (SO): Antimicrob. Agents Chemother., 38 (4), 648-652 (1994)

OTHER SOURCE (OS): CA 121:2236

REFERENCE: 21 (bases 150631 to 153085)

AUTHOR (AU): Legisa, M.; Bencina, M.

TITLE (TI): Evidence for the activation of 6-phosphofructo-1-kinase by cAMP-dependent protein kinase in Aspergillus niger

JOURNAL (SO): FEMS Microbiol. Lett., 118 (3), 327-333 (1994)

OTHER SOURCE (OS): CA 121:102759

REFERENCE: 22 (bases 138020 to 140061)

AUTHOR (AU): Kim, Y.J.; Bjorklund, S.; Li, Y.; Sayre, M.H.; Kornberg, R.D.

TITLE (TI): A multiprotein mediator of transcriptional activation and its interaction with the C-terminal repeat domain of RNA polymerase II

JOURNAL (SO): Cell, 77 (4), 599-608 (1994)

OTHER SOURCE (OS): CA 121:102149

REFERENCE: 23 (bases 38805 to 39836)

AUTHOR (AU): Downs, D.M.; Petersen, L.

TITLE (TI): apbA, a new genetic locus involved in thiamine biosynthesis in Salmonella typhimurium

JOURNAL (SO): J. Bacteriol., 176 (16), 4858-4864 (1994)

OTHER SOURCE (OS): CA 121:197350

REFERENCE: 24 (bases 5212 to 7379)

AUTHOR (AU): Li, Z.; Brendel, M.

TITLE (TI): Sensitivity to nitrogen mustard in Saccharomyces cerevisiae is independently determined by regulated choline permease and DNA repair

JOURNAL (SO): Mutat. Res., 315 (2), 139-145 (1994)

OTHER SOURCE (OS): CA 121:198201

REFERENCE: 25 (bases 85096 to 90863)

AUTHOR (AU): Szczypka, M.S.; Wemmie, J.A.; Moye-Rowley, W.S.; Thiele, D.J.

TITLE (TI): A yeast metal resistance protein similar to human cystic fibrosis transmembrane conductance regulator (CFTR) and multidrug resistance-associated protein

JOURNAL (SO): J. Biol. Chem., 269 (36), 22853-22857 (1994)

OTHER SOURCE (OS): CA 122:26140

REFERENCE: 26 (bases 91484 to 93088)

AUTHOR (AU): Knight, S.A.; Tamai, K.T.; Kosman, D.J.; Thiele, D.J.

TITLE (TI): Identification and analysis of a Saccharomyces cerevisiae copper homeostasis gene encoding a homeodomain protein

JOURNAL (SO): Mol. Cell. Biol., 14 (12), 7792-7804 (1994)

OTHER SOURCE (OS): CA 122:73697

REFERENCE: 27 (bases 85096 to 90863)

AUTHOR (AU): Wemmie, J.A.; Szczypka, M.S.; Thiele, D.J.; Moye-Rowley, W.S.

TITLE (TI): Cadmium tolerance mediated by the yeast AP-1 protein requires the presence of an ATP-binding cassette transporter-encoding gene, YCF1

JOURNAL (SO): J. Biol. Chem., 269 (51), 32592-32597 (1994)

OTHER SOURCE (OS): CA 121:294343

REFERENCE: 28 (bases 20773 to 22555)

AUTHOR (AU): Kamoda, S.; Saburi, Y.

TITLE (TI): Cloning of a lignostilbene-alpha,beta-dioxygenase isozyme gene from Pseudomonas paucimobilis TMY1009

JOURNAL (SO): Biosci. Biotechnol. Biochem., 59 (10), 1866-1868 (1995)

OTHER SOURCE (OS): CA 124:47043

REFERENCE: 29 (bases 85096 to 90863)

AUTHOR (AU): Li,Z.S.; Szczypka,M.; Lu,Y.P.; Thiele,D.J.; Rea,P.A.
 TITLE (TI): The yeast cadmium factor protein (YCF1) is a vacuolar glutathione S-conjugate pump
 JOURNAL (SO): J. Biol. Chem., 271 (11), 6509-6517 (1996)
 OTHER SOURCE (OS): CA 124:226108
 REFERENCE: 30 (bases 33419 to 35477)
 AUTHOR (AU): Silva,J.C.; Minto,R.E.; Barry,C.E. III; Holland,K.A.; Townsend,C.A.
 TITLE (TI): Isolation and characterization of the versicolorin B synthase gene from *Aspergillus parasiticus*. Expansion of the aflatoxin b1 biosynthetic gene cluster
 JOURNAL (SO): J. Biol. Chem., 271 (23), 13600-13608 (1996)
 OTHER SOURCE (OS): CA 125:50401
 REFERENCE: 31 (bases 15614 to 17392)
 AUTHOR (AU): Covert,S.F.; Enkerli,J.; Miao,V.P.; VanEtten,H.D.
 TITLE (TI): A gene for maackiain detoxification from a dispensable chromosome of *Nectria haematococca*
 JOURNAL (SO): Mol. Gen. Genet., 251 (4), 397-406 (1996)
 OTHER SOURCE (OS): CA 125:106677
 REFERENCE: 32 (bases 131646 to 132375)
 AUTHOR (AU): Mitsuhashi,S.; Miyachi,S.
 TITLE (TI): Amino acid sequence homology between N- and C-terminal halves of a carbonic anhydrase in *Porphyridium purpureum*, as deduced from the cloned cDNA
 JOURNAL (SO): J. Biol. Chem., 271 (45), 28703-28709 (1996)
 OTHER SOURCE (OS): CA 125:321312
 REFERENCE: 33 (bases 85096 to 90863)
 AUTHOR (AU): Li,Z.S.; Lu,Y.P.; Zhen,R.G.; Szczypka,M.; Thiele,D.J.; Rea,P.A.
 TITLE (TI): A new pathway for vacuolar cadmium sequestration in *Saccharomyces cerevisiae*: YCF1-catalyzed transport of bis(glutathionato)cadmium
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 94 (1), 42-47 (1997)
 OTHER SOURCE (OS): CA 126:127966
 REFERENCE: 34 (bases 1241 to 3043)
 AUTHOR (AU): Saito,Y.; Ishii,Y.; Hayashi,H.; Imao,Y.; Akashi,T.; Yoshikawa,K.; Noguchi,Y.; Soeda,S.; Yoshida,M.; Niwa,M.; Hosoda,J.; Shimomura,K.
 TITLE (TI): Cloning of genes coding for L-sorbose and L-sorbose dehydrogenases from *Gluconobacter oxydans* and microbial production of 2-keto-L-gulonate, a precursor of L-ascorbic acid, in a recombinant *G. oxydans* strain
 JOURNAL (SO): Appl. Environ. Microbiol., 63 (2), 454-460 (1997)
 OTHER SOURCE (OS): CA 126:167180
 REFERENCE: 35 (bases 150631 to 153085)
 AUTHOR (AU): Ruijter,G.J.; Panneman,H.; Visser,J.
 TITLE (TI): Overexpression of phosphofructokinase and pyruvate kinase in citric acid-producing *Aspergillus niger*
 JOURNAL (SO): Biochim. Biophys. Acta, 1334 (2-3), 317-326 (1997)
 OTHER SOURCE (OS): CA 126:222695
 REFERENCE: 36 (bases 49850 to 51919)
 AUTHOR (AU): Prieto,R.; Woloshuk,C.P.
 TITLE (TI): *ord1*, an oxidoreductase gene responsible for conversion of O-methylsterigmatocystin to aflatoxin in *Aspergillus flavus*
 JOURNAL (SO): Appl. Environ. Microbiol., 63 (5), 1661-1666 (1997)
 OTHER SOURCE (OS): CA 127:13942
 REFERENCE: 37 (bases 17766 to 20491)
 AUTHOR (AU): Todd,R.B.; Murphy,R.L.; Martin,H.M.; Sharp,J.A.; Davis,M.A.; Katz,M.E.; Hynes,M.J.
 TITLE (TI): The acetate regulatory gene *facB* of *Aspergillus nidulans* encodes a Zn(II)2Cys6 transcriptional

activator

JOURNAL (SO): Mol. Gen. Genet., 254 (5), 495-504 (1997)

OTHER SOURCE (OS): CA 127:105007

REFERENCE: 38 (bases 71863 to 73356)

AUTHOR (AU): Ballensiefen,W.; Schmitt,H.D.

TITLE (TI): Periplasmic Bar1 protease of *Saccharomyces cerevisiae* is active before reaching its extracellular destination

JOURNAL (SO): Eur. J. Biochem., 247 (1), 142-147 (1997)

OTHER SOURCE (OS): CA 127:187926

REFERENCE: 39 (bases 52148 to 53720)

AUTHOR (AU): Kuroyanagi,N.; Onogi,H.; Wakabayashi,T.; Hagiwara,M.

TITLE (TI): Novel SR-protein-specific kinase, SRPK2, disassembles nuclear speckles

JOURNAL (SO): Biochem. Biophys. Res. Commun., 242 (2), 357-364 (1998)

OTHER SOURCE (OS): CA 128:241040

REFERENCE: 40 (bases 113565 to 114733)

AUTHOR (AU): MacDiarmid,C.W.; Gardner,R.C.

TITLE (TI): Overexpression of the *Saccharomyces cerevisiae* magnesium transport system confers resistance to aluminum ion

JOURNAL (SO): J. Biol. Chem., 273 (3), 1727-1732 (1998)

OTHER SOURCE (OS): CA 128:177021

REFERENCE: 41 (bases 135940 to 137166)

AUTHOR (AU): Wang,H.Y.; Lin,W.; Dyck,J.A.; Yeakley,J.M.; Songyang,Z.; Cantley,L.C.; Fu,X.D.

TITLE (TI): SRPK2: a differentially expressed SR protein-specific kinase involved in mediating the interaction and localization of pre-mRNA splicing factors in mammalian cells

JOURNAL (SO): J. Cell Biol., 140 (4), 737-750 (1998)

OTHER SOURCE (OS): CA 128:306636

REFERENCE: 42 (bases 38805 to 39836)

AUTHOR (AU): Frodyma,M.E.; Downs,D.

TITLE (TI): ApbA, the ketopantoate reductase enzyme of *Salmonella typhimurium* is required for the synthesis of thiamine via the alternative pyrimidine biosynthetic pathway

JOURNAL (SO): J. Biol. Chem., 273 (10), 5572-5576 (1998)

OTHER SOURCE (OS): CA 128:305459

REFERENCE: 43 (bases 106231 to 106803)

AUTHOR (AU): Woloshuk,C.P.; Prieto,R.

TITLE (TI): Genetic organization and function of the aflatoxin B1 biosynthetic genes

JOURNAL (SO): FEMS Microbiol. Lett., 160 (2), 169-176 (1998)

OTHER SOURCE (OS): CA 128:290649

REFERENCE: 44 (bases 93571 to 94963)

AUTHOR (AU): Philp,N.J.; Yoon,H.; Grollman,E.F.

TITLE (TI): Monocarboxylate transporter MCT1 is located in the apical membrane and MCT3 in the basal membrane of rat RPE

JOURNAL (SO): Am. J. Physiol., 274 (6 PT 2), R1824-R1828 (1998)

OTHER SOURCE (OS): CA 129:159493

REFERENCE: 45 (bases 93571 to 94963)

AUTHOR (AU): Wilson,M.C.; Jackson,V.N.; Heddle,C.; Price,N.T.; Pilegaard,H.; Juel,C.; Bonen,A.; Montgomery,I.; Hutter,O.F.; Halestrap,A.P.

TITLE (TI): Lactic acid efflux from white skeletal muscle is catalyzed by the monocarboxylate transporter isoform MCT3

JOURNAL (SO): J. Biol. Chem., 273 (26), 15920-15926 (1998)

OTHER SOURCE (OS): CA 129:159801

REFERENCE: 46 (bases 153410 to 154508)

AUTHOR (AU): Dekkers,L.C.; van der Bij,A.J.; Mulders,I.H.;

Phoelich, C.C.; Wentwoord, R.A.; Glandorf, D.C.;
Wijffelman, C.A.; Lugtenberg, B.J.

TITLE (TI): Role of the O-antigen of lipopolysaccharide, and
possible roles of growth rate and of NADH:ubiquinone
oxidoreductase (nuo) in competitive tomato root-tip
colonization by *Pseudomonas fluorescens* WCS365

JOURNAL (SO): Mol. Plant Microbe Interact., 11 (8), 763-771 (1998)

OTHER SOURCE (OS): CA 129:200426

REFERENCE: 47 (bases 146433 to 148685)

AUTHOR (AU): Saito, K.; Yamazaki, H.; Ohnishi, Y.; Fujimoto, S.;
Takahashi, E.; Horinouchi, S.

TITLE (TI): Production of trehalose synthase from a basidiomycete,
Grifola frondosa, in *Escherichia coli*

JOURNAL (SO): Appl. Microbiol. Biotechnol., 50 (2), 193-198 (1998)

OTHER SOURCE (OS): CA 130:956

REFERENCE: 48 (bases 122486 to 123895)

AUTHOR (AU): Kimura, M.; Matsumoto, G.; Shingu, Y.; Yoneyama, K.;
Yamaguchi, I.

TITLE (TI): The mystery of the trichothecene 3-O-acetyltransferase
gene. Analysis of the region around Tri101 and
characterization of its homologue from *Fusarium*
sporotrichioides

JOURNAL (SO): FEBS Lett., 435 (2-3), 163-168 (1998)

OTHER SOURCE (OS): CA 130:11163

REFERENCE: 49 (bases 146433 to 148685)

AUTHOR (AU): Saito, K.; Kase, T.; Takahashi, E.; Horinouchi, S.

TITLE (TI): Purification and characterization of a trehalose
synthase from the basidiomycete *grifola frondosa*

JOURNAL (SO): Appl. Environ. Microbiol., 64 (11), 4340-4345 (1998)

OTHER SOURCE (OS): CA 130:34870

REFERENCE: 50 (bases 14029 to 15172)

AUTHOR (AU): Feng, Y.; Khoo, H.E.; Poh, C.L.

TITLE (TI): Purification and characterization of gentisate
1,2-dioxygenases from *Pseudomonas alcaligenes* NCIB 9867
and *Pseudomonas putida* NCIB 9869

JOURNAL (SO): Appl. Environ. Microbiol., 65 (3), 946-950 (1999)

OTHER SOURCE (OS): CA 130:322223

REFERENCE: 51 (bases 59070 to 60560)

AUTHOR (AU): Bosch, R.; Moore, E.R.; Garcia-Valdes, E.; Pieper, D.H.

TITLE (TI): NahW, a novel, inducible salicylate hydroxylase
involved in mineralization of naphthalene by
Pseudomonas stutzeri AN10

JOURNAL (SO): J. Bacteriol., 181 (8), 2315-2322 (1999)

OTHER SOURCE (OS): CA 131:70144

REFERENCE: 52

AUTHOR (AU): DeZwaan, T.M.; Carroll, A.M.; Valent, B.; Sweigard, J.A.

TITLE (TI): Magnaporthe grisea pth11p is a novel plasma membrane
protein that mediates appressorium differentiation in
response to inductive substrate cues

JOURNAL (SO): Plant Cell, 11 (10), 2013-2030 (1999)

OTHER SOURCE (OS): CA 132:47358

REFERENCE: 53 (bases 122486 to 123895)

AUTHOR (AU): McCormick, S.P.; Alexander, N.J.; Trapp, S.E.; Hohn, T.M.

TITLE (TI): Disruption of TRI101, the gene encoding trichothecene
3-O-acetyltransferase, from *Fusarium sporotrichioides*

JOURNAL (SO): Appl. Environ. Microbiol., 65 (12), 5252-5256 (1999)

OTHER SOURCE (OS): CA 132:118174

REFERENCE: 54 (bases 111907 to 113460)

AUTHOR (AU): Muraguchi, H.; Kamada, T.

TITLE (TI): A mutation in the eln2 gene encoding a cytochrome P450
of *Coprinus cinereus* affects mushroom morphogenesis

JOURNAL (SO): Fungal Genet. Biol., 29 (1), 49-59 (2000)

OTHER SOURCE (OS): CA 134:96073

REFERENCE: 55 (bases 108826 to 111209)

AUTHOR (AU): Yu, J.; Chang, P.K.; Bhatnagar, D.; Cleveland, T.E.

TITLE (TI): Genes encoding cytochrome P450 and monooxygenase enzymes define one end of the aflatoxin pathway gene cluster in *Aspergillus parasiticus*

JOURNAL (SO): Appl. Microbiol. Biotechnol., 53 (5), 583-590 (2000)

OTHER SOURCE (OS): CA 133:291807

REFERENCE: 56 (bases 122486 to 123895)

AUTHOR (AU): Muhitch, M.J.; McCormick, S.P.; Alexander, N.J.; Hohn, T.M.

TITLE (TI): Transgenic expression of the TRI101 or PDR5 gene increases resistance of tobacco to the phytotoxic effects of the trichothecene 4,15-diacetoxyscirpenol

JOURNAL (SO): Plant Sci., 157 (2), 201-207 (2000)

OTHER SOURCE (OS): CA 133:306551

REFERENCE: 57 (bases 107279 to 108340)

AUTHOR (AU): Cheng, Q.; Thomas, S.M.; Kostichka, K.; Valentine, J.R.; Nagarajan, V.

TITLE (TI): Genetic analysis of a gene cluster for cyclohexanol oxidation in *Acinetobacter* sp. Strain SE19 by in vitro transposition

JOURNAL (SO): J. Bacteriol., 182 (17), 4744-4751 (2000)

OTHER SOURCE (OS): CA 134:37832

REFERENCE: 58 (bases 100363 to 101496)

AUTHOR (AU): Jornvall, H.; Hoog, J.O.; Persson, B.; Pares, X.

TITLE (TI): Pharmacogenetics of the alcohol dehydrogenase system

JOURNAL (SO): Pharmacology, 61 (3), 184-191 (2000)

OTHER SOURCE (OS): CA 134:38655

REFERENCE: 59

AUTHOR (AU): Calabrese, D.; Bille, J.; Sanglard, D.

TITLE (TI): A novel multidrug efflux transporter gene of the major facilitator superfamily from *Candida albicans* (FLU1) conferring resistance to fluconazole

JOURNAL (SO): Microbiology (Reading, Engl.), 146 (PT 11), 2743-2754 (2000)

OTHER SOURCE (OS): CA 135:1055

REFERENCE: 60

AUTHOR (AU): Deising, H.B.; Werner, S.; Wernitz, M.

TITLE (TI): The role of fungal appressoria in plant infection

JOURNAL (SO): Microbes Infect., 2 (13), 1631-1641 (2000)

REFERENCE: 61 (bases 43783 to 45994)

AUTHOR (AU): Smith, S.

TITLE (TI): The world according to PARP

JOURNAL (SO): Trends Biochem. Sci., 26 (3), 174-179 (2001)

OTHER SOURCE (OS): CA 135:15779

REFERENCE: 62 (bases 131646 to 132375)

AUTHOR (AU): Cronk, J.D.; Endrizzi, J.A.; Cronk, M.R.; O'Neill, J.W.; Zhang, K.Y.

TITLE (TI): Crystal structure of *E. coli* beta-carbonic anhydrase, an enzyme with an unusual pH-dependent activity

JOURNAL (SO): Protein Sci., 10 (5), 911-922 (2001)

REFERENCE: 63 (bases 43783 to 45994)

AUTHOR (AU): Ziegler, M.; Oei, S.L.

TITLE (TI): A cellular survival switch: poly(ADP-ribosyl)ation stimulates DNA repair and silences transcription

JOURNAL (SO): Bioessays, 23 (6), 543-548 (2001)

REFERENCE: 64 (bases 43783 to 45994)

AUTHOR (AU): Herceg, Z.; Wang, Z.Q.

TITLE (TI): Functions of poly(ADP-ribose) polymerase (PARP) in DNA repair, genomic integrity and cell death

JOURNAL (SO): Mutat. Res., 477 (1-2), 97-110 (2001)

OTHER SOURCE (OS): CA 136:145570

REFERENCE: 65 (bases 15614 to 17392)
 AUTHOR (AU): Mundodi, S.R.; Watson, B.S.; Lopez-Meyer, M.; Paiva, N.L.
 TITLE (TI): Functional expression and subcellular localization of
 the *Nectria haematococca* Mak1 phytoalexin
 detoxification enzyme in transgenic tobacco
 JOURNAL (SO): Plant Mol. Biol., 46 (4), 421-432 (2001)
 OTHER SOURCE (OS): CA 135:285870
 REFERENCE: 66 (bases 1 to 163680)
 AUTHOR (AU): Pel, H.J.; de Winde, J.H.; Archer, D.B.; Dyer, P.S.;
 Hofmann, G.; Schaap, P.J.; Turner, G.; de Vries, R.P.;
 Albang, R.; Albermann, K.; Andersen, M.R.; Bendtsen, J.D.;
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 Vervecken, W.; van de Vondervoort, P.J.; Wedler, H.;
 Wosten, H.A.; Zeng, A.P.; van Ooyen, A.J.; Visser, J.;
 Stam, H.
 TITLE (TI): Genome sequencing and analysis of the versatile cell
 factory *Aspergillus niger* CBS 513.88
 JOURNAL (SO): Nat. Biotechnol., 25 (2), 221-231 (2007)
 OTHER SOURCE (OS): CA 146:310276
 REFERENCE: 67 (bases 1 to 163680)
 AUTHOR (AU): Pel, H.J.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O.
 Box 1, 2600 MA Delft, THE NETHERLANDS

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 Regulation: in *S. cerevisiae*,
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 precursors inositol and choline
 and this regulation involves the
 trans-acting factors Ino2p, Ino4p
 and Opilp. Remark: alternate name
 for *S. cerevisiae* Hnml is YGL077c.
 Similarity: Hnml of *S. cerevisiae*
 belongs to the APC family, which
 encompasses amino acid permeases
 more related to the mammalian
 cationic amino-acid transporter
 family (Tea/ecoR). Title: strong
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exon	complement(5746..6075)	/locus-tag="An18g00960" /number=3
intron	complement(6076..6139)	/locus-tag="An18g00960" /number=3
exon	complement(6140..6159)	/locus-tag="An18g00960" /number=4
intron	complement(6160..6224)	/locus-tag="An18g00960" /number=4
exon	complement(6225..6602)	/locus-tag="An18g00960" /number=5
intron	complement(6603..6673)	/locus-tag="An18g00960" /number=5
exon	complement(6674..6746)	/locus-tag="An18g00960"

intron	complement(6747..6799)	/number=6 /locus-tag="An18g00960" /number=6
exon	complement(6800..6899)	/locus-tag="An18g00960" /number=7
intron	complement(6900..7248)	/locus-tag="An18g00960" /number=7
exon	complement(7249..7379)	/locus-tag="An18g00960" /number=8
gene	complement(<7770..>8415)	/locus-tag="An18g00970"
mRNA	complement(join(<7770.. 8282,8380..>8415))	/locus-tag="An18g00970"
CDS	complement(join(7770..8 282,8380..8415))	/locus-tag="An18g00970"
		/note="unnamed protein product; Title: weak similarity to hypothetical protein BAA96207.1 - Oryza sativa" /codon-start=1 /protein-id="CAK47174.1" /db-xref="GI:134084141" /translation="MLCTHAGGEGARSGRPDDRQ GHQPISVALWLCAPPPGFLSGRTS LASAGISNPDGATAVNTCETVGCLGLTACGQDCL SSRAALAEALLLGLCCVGDGGGRA PANPNKMDRYLLLYCRLGLTLDGPIVVVVVHTLS LSCSPPTQLHPPPLLASLHSFFPP ESLGRVPISIIYAHMRHAAAKIV"
exon	complement(7770..8282)	/locus-tag="An18g00970" /number=1
intron	complement(8283..8379)	/locus-tag="An18g00970" /number=1
exon	complement(8380..8415)	/locus-tag="An18g00970" /number=2
gene	<8621..>9700	/locus-tag="An18g00980"
mRNA	join(<8621..8764, 8830..9156,9214..9356, 9406..>9700)	/locus-tag="An18g00980"
CDS	join(8621..8764, 8830..9156,9214..9356, 9406..9700)	/locus-tag="An18g00980"
		/note="unnamed protein product; Function: M. grisea Pth11 is a pathogenicity gene. Function: M. grisea Pth11p is likely to be involved in host surface recognition. Function: M. grisea pth11 mutants of strain 4091-5-8 are nonpathogenic due to a defect in appressorium differentiation. Localization: in M. grisea, a Pth11-green fluorescent protein fusion localised to the cell membrane and vacuoles. Similarity: similarity of the predicted A. niger protein and M. grisea Pth11 is limited to the N-terminal half of the protein sequences. Title: weak similarity to integral membrane protein PTH11 - Magnaporthe grisea plasma

		membrane"
		/citation=[52]
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		/protein-id="CAK47175.1"
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		/translation="MTDHSAAVKVVTCTLLIVSF
		IAVVACLTNNWQVLRKVSSVALL
		LSTLIASIASGAAVSVAATHGLGQASPLTDAQVV
		VMQKALYSMEVLYVLTGLGLKLSV
		MVLFYSLLSSTGQSKSVLAATGLLLIWVVVMVIV
		VCLQCHPPEVWNIVGGTCLDLGI
		WIAFGVMNVLVEIMIIAVPSFIIIFRLKLSLKRRLL
		VVISCFGIRILDIAGSIVQLCYVR
		NFKIHADSPMPTNVWQWAICSQVLQTVAILSACV
		PYLREFLESFPGMFKPTELKHPT
		VQSAYNATKCSDSIELMRPESTKDT"
sig-peptide	8621..8698	/locus-tag="An18g00980"
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mat-peptide	join(8699..8764, 8830..9156,9214..9356, 9406..9697)	/locus-tag="An18g00980"
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intron	8765..8829	/locus-tag="An18g00980"
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intron	9157..9213	/locus-tag="An18g00980"
		/number=2
exon	9214..9356	/locus-tag="An18g00980"
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intron	9357..9405	/locus-tag="An18g00980"
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exon	9406..9700	/locus-tag="An18g00980"
		/number=4
gene	complement(<9787..>9927	/locus-tag="An18g00990"
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mRNA	complement(<9787..>9927	/locus-tag="An18g00990"
)	
CDS	complement(9787..9927)	/locus-tag="An18g00990"
		/note="unnamed protein product;
		Title: strong similarity to EST
		an-1359 -Aspergillus niger"
		/codon-start=1
		/protein-id="CAK47176.1"
		/db-xref="GI:134084143"
		/translation="MRAATLLLVALLSAVALALPT
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sig-peptide	complement(9877..9927)	/locus-tag="An18g00990"
		/inference="protein
		motif:SignalP:2.0"
mat-peptide	complement(9790..9876)	/locus-tag="An18g00990"
		/product="unnamed"
exon	complement(9787..9927)	/locus-tag="An18g00990"
		/number=1
gene	<10500..>11479	/locus-tag="An18g01000"
mRNA	join(<10500..10749, 10812..11041, 11105..>11479)	/locus-tag="An18g01000"
CDS	join(10500..10749,	/locus-tag="An18g01000"

10812..11041,
11105..11479)

		/note="unnamed protein product; Similarity: the nucleotide sequence of the ORF shows strong similarity to the ESTs an-2192 and an-2204 of <i>A. niger</i> . Title: strong similarity to EST an-2192 - <i>Aspergillus niger</i> " /codon-start=1 /protein-id="CAK47177.1" /db-xref="GI:134084144" /translation="MYSYEKVNRRDDSDQGLLAE DSERVAPQPRVSRFPSWTNALLLL GLLFSLSLNVGWVFQKGHNVP IQDLDPDAAMAK QRSPYTGLAWDTHKPYSHHSEYTS ENATHADEMWESLSMDPMVIAPTWEWAQSKGLSD SWAFPWDSNRRIYFIKVFHQLHCL KLMRHSYHELWSGQESSIPAPHIEHCLDSL RQDL MCKADDTMPPSLQLLNGGGEGQQM QCKDFDKLVAWSKAPERNACYKRLTDYKPIVHSI ERYAFCPEDSEHYPTMSKYFEEHG HYADPFSE"
exon	10500..10749	/locus-tag="An18g01000" /number=1
intron	10750..10811	/locus-tag="An18g01000" /number=1
exon	10812..11041	/locus-tag="An18g01000" /number=2
intron	11042..11104	/locus-tag="An18g01000" /number=2
exon	11105..11479	/locus-tag="An18g01000" /number=3
gene	<11980..>13464	/locus-tag="An18g01010"
mRNA	join(<11980..12137, 12198..>13464)	/locus-tag="An18g01010"
CDS	join(11980..12137, 12198..13464)	/locus-tag="An18g01010"
		/inference="profile:COGS:COG0477" /note="unnamed protein product; Function: FLU1 of <i>C. albicans</i> facilitates resistance to fluconazole and cycloheximide in the fluconazole-hypersensitive <i>S.</i> <i>cerevisiae</i> strain YKKB-13 lacking the ABC (ATP-binding cassette) transporter gene PDR5. Function: FLU1 of <i>C. albicans</i> facilitates resistance to mycophenolic acid in <i>C. albicans</i> . Function: FLU1 of <i>C.</i> <i>albicans</i> is involved in the resistance to azol derivatives in <i>C. albicans</i> . Function: MDR1 of <i>C.</i> <i>albicans</i> facilitates resistance to the anti-mitotic drug benomyl and to the dihydrofolate reductase inhibitor methotrexate. Similarity: N-terminus of the <i>A.</i> <i>niger</i> protein is app. 120 aa shorter than in FLU1 of <i>C.</i> <i>albicans</i> . Similarity: the predicted <i>A. niger</i> protein shows strong similarity to fluconazole

resistance protein FLU1 of *C. albicans*, which is a permease belonging to the major facilitator superfamily. Title: strong similarity to fluconazole resistance protein FLU1 - *Candida albicans*"

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 RTLIVSIWELGEIVAPLLWGPLSE
 LYGRQWPLNIANLFFVAFLAGTAASTSIQMLIAF
 RFLSGAATAASAIGPGIVSDFPE
 ESRGRAMSIMSLTGALGPVVGPIIGSYLGEKAGW
 RWAFLPTIATGTLSLLILVVYRE
 TYSVTLQKRKARQQNPESGSKSPEDTDKTASQVF
 FKAILRPLRLLIRSPMLILVTFYL
 SVVYGYTYLVMTTIAPLFQDVYGFSEGLAFL
 GLCLGLILGAFLCSFLLDRYVRTA
 RARSGTSKPEQRLPPVLIACFVMSGGLFLFGWTA
 QYHVQWIAPIIGTGIIIGFLVSTT
 ITLQTYVVDLFGIYAASATSAMLVPRNACAAFLP
 LAGPPLFDRLGYNWGGTLLALIVL
 VFSLMPLIFINYGERLRGKNLLDD"

exon 11980..12137

/locus-tag="An18g01010"
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intron 12138..12197

/locus-tag="An18g01010"
 /number=1

exon 12198..13464

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 /number=2

gene complement(<14029..>15172)

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mRNA complement(join(<14029..
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 14917..>15172))

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CDS complement(join(14029..
 14318,14411..14845,
 14917..15172))

/locus-tag="An18g01020"
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 /inference="profile:COGS:COG3435"
 /inference="similar to AA
 sequence:UniProtKB:AF173167.3"
 /note="unnamed protein product;
 Complex: the estimated molecular
 mass of the purified gentisate 1,
 2-dioxygenase of *P. alcaligenes*
 was 154 kDa, with a subunit mass
 of 39 kDa. its structure is
 deduced to be a tetramer. Remark:
 gentisate 1,2-dioxygenase of *P.*
alcaligenes exhibits typical
 saturation kinetics and has an
 apparent Km of 92 microM for
 gentisate. this enzyme has broad
 substrate specificities towards
 alkyl and halogenated gentisate
 analogs. Similarity: the predicted
A. niger protein shows strong

```

similarity to gentisate
1,2-dioxygenase of P. alcaligenes
and conserved hypothetical
proteins from other procaryotic
species. Title: strong similarity
to gentisate 1,2-dioxygenases xlnE
- Pseudomonas alcaligenes"
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PTAVPFIWRYDSIRPNLLRAGELVTEKQAERRVL
MLVNPARDAPYTTDTLYAGLQLVM
PNETAPAHRHTAFAMRYIIIEGNGGFTAVHGKRIK
MQKGDVILTPTWNYHDHGKDGTP
MIWLDGLDLPNFRHFPVHFVDHYDQPRYPADVD
SATSPIVFPWDKMKAELDKAPGTW
AVRRYL RADGSEGGS AERVDAGTSSLPRQET TSA
VYHVIAGSGCSEIGDKTLVWETGD
TFCVPSWYKYRHIAAEGETVYLYRFDDKPMISAL
GFYRSIDTDLATLVSQ"
exon      complement(14029..14318 /locus-tag="An18g01020"
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                                     /number=1
intron    complement(14319..14410 /locus-tag="An18g01020"
)
                                     /number=1
exon      complement(14411..14845 /locus-tag="An18g01020"
)
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intron    complement(14846..14916 /locus-tag="An18g01020"
)
                                     /number=2
exon      complement(14917..15172 /locus-tag="An18g01020"
)
                                     /number=3
gene      <15614..>17392           /locus-tag="An18g01030"
mRNA      join(<15614..15661,    /locus-tag="An18g01030"
15723..16281,
16347..16503,
16584..16739,
16803..16942,
17034..>17392)
CDS       join(15614..15661,    /locus-tag="An18g01030"
15723..16281,
16347..16503,
16584..16739,
16803..16942,
17034..17392)

/inference="profile:COGS:COG0654"
/inference="profile:PFAM:PF01360"
/note="unnamed protein product;
Function: Mak1 from N.
haematococca specifically
hydroxylates the phytoalexins
medicarpin and
maackiain, converting them to less
fungitoxic derivatives.
Localization: heterologous
expression of the Mak1 cDNA

```

construct in plants indicated that Mak1 protein accumulates in the plant cytoplasm, associated with endoplasmic reticulum membranes. Similarity: the predicted A. niger protein shows strong similarity to Mak1 from the fungal pathogen N. haematococca. Mak1 belongs to the flavin-containing mono-oxygenases. best matches are with putative salicylate hydroxylases of several procaryotic species. Title: strong similarity to maackiain detoxification protein 1 MAK1 - Nectria haematococca endoplasmatic reticulum"

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 TPVLGEVGAGIQIPSNSTRILFSL
 GLQSYLEPYVTAPESISFRRWQNGKVI GLTKLIP
 NFVNNFKAPYYVIHRADFHSALCQ
 KALDVGVEIELGAKVVDYDPIVGSITLADGTKHS
 ADLIVAADGIKSVARNVVLQGD
 EM RFQGGPGFAAYRAVVDVGKMRRDPDLSWILEK
 PAL NIWIGDSRHVMTYTIGAGKAFNMV
 LSHPEMTDPGTWKPETALEDMKA EFQGWDPILSK
 IIGMVEKTVKWPLLTGTLLQNWTV
 GKLVI LGDAAHAMVPYMSQGAAMAVEDGIALSRS
 LSHMTSRDQLQKALSIFQEVRKKR
 AGHMQEASLLNGKLWHFPDGS LQQARDEAMAPEV
 QGIPF SHSPNQWSDPATQMW CYGY
 DAEEAIDIAWMESLEARVDCVH"

exon	15614..15661
intron	15662..15722
exon	15723..16281
intron	16282..16346
exon	16347..16503
intron	16504..16583
exon	16584..16739
intron	16740..16802
exon	16803..16942
intron	16943..17033
exon	17034..17392
gene	<17766..>20491
mRNA	join(<17766..17864,

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CDS

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18398..19163,  
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20325..>20491)  
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18398..19163,  
19373..19935,  
20037..20252,  
20325..20491)  
  
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/inference="similar to AA  
sequence:UniProtKB:ENU56097.1"  
/note="unnamed protein product;  
Phenotype: facB recessive loss of  
function mutants in A. nidulans  
are deficient in acetate induction  
of acetyl-CoA synthase, isocitrate  
lyase, malate  
synthase, acetamidase, and  
NADP-isocitrate dehydrogenase.  
Similarity: the predicted A. niger  
protein shows similarity to  
acetate regulatory DNA binding  
protein FacB (facB) from A.  
nidulans, which belongs to the  
GAL4-type zinc cluster  
transcriptional activators. Title:  
similarity to acetate regulatory  
DNA binding protein facB -  
Aspergillus nidulans"  
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DAPRKENPLSNQSERFSDFAGTEDTIDAMGAVAF  
ADEEDCGFFGPSSNIAFLRHLSCA  
VAHSASAQKEITSPPLDRVAYDGGFVSATRPSSP  
SHDQRPESLEGEKFDKFALPPPEE  
SLALIHRYFADTGLLFPYIHPPTFFETYAELKDN  
SKRVRRTWLGLLNIIILAMAKLTAV  
SGTTSAETGISESAIYYHRALSLCKGEILRGTTL  
EVGRYSIYAPVRARVPVYLRATKI  
NTVQYLLVMGQYLQGTQKSVQAWTIHGLAVKAAL  
QLGLHSGKASRAFTPLEQEVKRKT  
WFGCVVLDVRANLFLNRKTIQQANIRVSTLYK  
QIANIIDRIYGQNLGCDSPLSIGE  
TVGRVLGIENQLFSWVLGLPESLRQVTVQSMREE  
IERSEVGDEGHHKLYPLKFRIILT  
LRYFHVQILLHRPILVKFLDATGPSGLEADEVKL  
LNDIGYSSMNKCVDSAMGIIDIIH  
ELVSTTGWQKDLLGAWWYSLYYTFNAALVIIGAM  
WVQRNRDTSDEPVDNGGNNNNMDI  
YLSRAVLTLQNLNVGNRMVDRCKYYLDQLITLLG  
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		/number=6
intron	20253..20324	/locus-tag="An18g01040"
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		/number=7
gene	complement(<20773..>225	/locus-tag="An18g01050"
	55)	
mRNA	complement(join(<20773.	/locus-tag="An18g01050"
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	21710..22119,	
	22180..22303,	
	22370..>22555))	
CDS	complement(join(20773..	/locus-tag="An18g01050"
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	21710..22119,	
	22180..22303,	
	22370..22555))	
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		/inference="profile:COGS:COG3670"
		/inference="profile:PFAM:PF03055"
		/inference="similar to AA
		sequence:PIR:JC4324"
		/note="unnamed protein product;
		Catalytic activity:
		lignostilbene-alpha,beta-dioxygena
		se isozymes (LSD-I, II, and III)
		of P. paucimobilis catalyse the
		reaction
		1,2-bis(4-hydroxy-3-methoxyphenyl)
		ethylene + O(2) = 2 vanillin
		Cofactor:
		lignostilbene-alpha,beta-dioxygena
		se isozymes (LSD-I, II, and III)
		of P. paucimobilis require iron as
		a cofactor. Complex: LSD-I, II,
		and III consist of alpha
		alpha,alpha beta, and beta beta
		subunits, respectively. they show
		different specificities for
		several substrates that are

stilbene and styrene derivatives.
Function: LSD of *P. paucimobilis*
catalyses the oxidative cleavage
of the interphenyl double bond in
the synthetic substrate and
lignin-derived stilbenes. it is
responsible for the degradation of
a diarylpropane-type structure in
lignin. Similarity: the predicted
A. niger protein shows strong
similarity to subunit lsdB of
lignostilbene-alpha,beta-dioxygena
se isozyme LSD-III of *P.*
paucimobilis and related
dioxygenases from several plant
species. Title: strong similarity
to subunit lsdB of
lignostilbene-alpha,beta-dioxygena
se isozyme LSD-III -*Pseudomonas*
paucimobilis"
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/citation=[28]
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RVSFQQRYVRTEKFVRERQAQRAL
IAQLTLFLWSIEGKYRNKFTDAVEFKVRSTANTN
IVYFNGQLLALKEDSPPYAMPDVT
LETRGLYDFDGQLPSMTFTAHPKFDPETGEMICF
GYEARGDGTDPVCYYTVGPDGKFT
EVVWLVPVVMIIHDFAVTDNWVIFPIIPQLCDI
ERMKQGGEHWQWSPETPLYLGVIP
RRGAKTADVKKWFQYKNSFPGHTANAHEDSSGNLI
IDLGLSEKNVFFWWPDAQGNAPEP
SSIRSQLVRFTINPRAEDLNLTEPRILQADNSEF
YRIDDRYATKPHRHVFFDMMDP
SL
GTDFARIAPVLGGGYPLYNSLARFDNVTGETEVY
FPGKTHMVQEPVFI PRSELAAEGD
GYLLALVNNYDSMSSELHLLDTADFTRARAKILL
PVRLRPGLHGSWVDGSDVPLSAAR L"

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		/number=2
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gene	<23096..>24052	/number=5 /locus-tag="An18g01060"
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gene	<24984..>27426	/number=3 /locus-tag="An18g01070"
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                Catalytic activity:
                lysophospholipase catalyses the
                reaction 2-lysophosphatidylcholine
                + H(2)O = glycerophosphocholine +
                a fatty acid anion. Pathway:
                lysophospholipase is involved in
                phospholipid degradation.
                Similarity: the predicted A. niger
                protein shows strong similarity to
                the protein sequences
                lysophospholipase (sequence 5 and
                sequence 7) of patents
                WO0127251-A/5 and WO0127251-A/7
                from A. oryzae (AC# AX112082 and
                AC# AX112084) and to other fungal
                lysophospholipases. Title: strong
                similarity to lysophospholipase
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the function of the protein.
 Similarity: the predicted A. niger
 protein shows strong similarity to
 the protein sequence alcohol
 dehydrogenase (sequence 19) of
 patent EP0845532-A/19 from an
 unclassified organism (AC# A92108)
 and to other zinc-containing
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          Catalytic activity: versicolorin B
          synthase from A. parasiticus
          catalyses the side chain
          cyclization of racemic versiconal
          hemiacetal to the bisfuran ring
          system of(-)-versicolorin B.
          Pathway: versicolorin B synthase
          from A. parasiticus is involved in
          the aflatoxin biosynthetic
          pathway. Remark: a splice site was
          detected upstream of the START
          codon. Remark: aflatoxins comprise
          a group of polyketide-derived
          carcinogenic mycotoxins. Remark:
          the genes encoding the aflatoxin
          biosynthetic enzymes in A.
          parasiticus are clustered. Remark:
          versicolorin B synthase from A.
          parasiticus possesses an
          amino-terminal sequence homologous
          to the ADP-binding region of other
          flavoenzymes, but does not require
          flavin or nicotinamide cofactors
          for its cyclase activity.
          Similarity: the predicted A. niger
          protein shows strong similarity to
          versicolorin B synthase from A.
          parasiticus and other
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		51484) of patent EP1033405-A2 from A. thaliana (AC# AAG41385) and to putative sterol desaturase family proteins. Title: similarity to protein fragment SEQ ID NO:51484 from patent EP1033405-A2 - Arabidopsis thaliana" /codon-start=1 /protein-id="CAK47190.1" /db-xref="GI:134084157" /translation="MSGTHPNPKDSMKSTWRRLD RAEWTIYHWFYEILGVHPEHLDKE VPVHQKTEKIPYMRTWSQHVWILYHAFIPLAVHH VYVSYTGQNFTPVGAFFFYISIAFK LIAIHQLQVMRRMGHVLGFLDGDQHGVDGVPDVG VAKVVRSLISTSTFRPIMTVFLSY RVSQAPAQMSWGWLPLEIGLYGIILDFWFYWYHR LMHDVGSGLWKYHRTTHLTKHPNPL LTLYADTEQEFFDIAGIPLMTYFSMRLMGMPMGF YEWWICHQYVVFTELAGHSGLRMH ASPPSTLDWLLRLIGAELVIEDHDLHHRKGWKKS HNYGKQTRLWDKIFGTCHERIESR EGNVDYDNTVRMPIF"
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facilitates resistance to
fluconazole and cycloheximide in
the fluconazole-hypersensitive S.
cerevisiae strain YKKB-13 lacking
the ABC (ATP-binding cassette)
transporter gene PDR5. Function:
FLU1 of C. albicans facilitates
resistance to mycophenolic acid in
C. albicans. Function: FLU1 of C.
albicans is involved in the
resistance to azol derivatives in
C. albicans. Function: MDR1 of C.
albicans facilitates resistance to
the anti-mitotic drug benomyl and
to the dihydrofolate reductase
inhibitor methotrexate.
Similarity: the predicted A. niger
protein shows strong similarity to
fluconazole resistance protein
FLU1 of C. albicans, which is a
permease belonging to the major
facilitator superfamily. Title:
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exon

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CDS	join(43783..43852, 43912..44025, 44075..44344, 44395..45240, 45294..45376, 45425..45994)	/locus-tag="An18g01170"

/EC-number="2.4.2.30"
 /inference="profile:PFAM:PF00644"
 /inference="profile:PFAM:PF02877"
 /note="unnamed protein product;
 Catalytic activity: the NAP
 protein of Z. mays catalyses the
 reaction NAD(+) +
 {ADP-D-ribosyl}(N)-acceptor <=>
 nicotinamide +
 {ADP-D-ribosyl}(N+1)-acceptor.
 Function: the NAP protein of Z.
 mays is involved in programmed
 cell death or apoptosis.
 Localization: the NAP protein of
 Z. mays is a nuclear enzyme.
 Remark: the ADP-D-ribosyl group of
 NAD(+) is transferred to an
 acceptor carboxyl group on a
 histone or the enzyme itself, and
 further ADP-ribosyl groups are
 transferred to the 2'-position of
 the terminal adenosine moiety,
 building up a polymer with an
 average chain length of 20-30
 units. Remark: the NAP
 polynucleotide sequences can be
 used for modulation of programmed
 cell death in eukaryotic cells.
 the method is used, specifically
 in plants, to induce, or protect
 against, programmed cell
 death, depending on the extent to
 which PARP activity is reduced.

reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc. , or during transformation). particular applications are generation of plants that are resistant to fungi or nematodes; are male or female sterile ; or have better seed-shatter properties. the methods are also used to improve growth of transformed plant cells (and derived calli or complete plants). Similarity: the predicted A. niger protein shows strong similarity to the protein sequence poly(ADP-ribose) polymerase NAP protein of patent WO200004173-A1 from Z. mays (AC# AAY68834) and from many other eucaryotic organisms. Title: strong similarity to poly(ADP-ribose) polymerase NAP protein from patent WO200004173-A1 - Zea mays nucleus"

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 DDEPESPKKRTLEQALGINEDGTTKKLKDAQTVG
 TKQINVPVDDTCPLRLTFTVYIDP
 TGLIWDATLNQTSATNNNNKFYRIQLLHRNNEFR
 TWTHWGRVGEHQHALLGGGGLDE
 AEYEFKKKFKDKSGLTWENRLDPPKKGKYTFIEK
 NYEEDTEDEDEDEDKVVAKKPTKP
 KAEVVKCTLSAPVQDLVSFIFNKDFQSTMASMS
 YDAQKLPLGKLSKRTLQNGFQALK
 DLSELIANPALASTKYDTSFTAAVEHLSNLYFTV
 IPHAFGRNRPPVLNNDNLLKREIE
 LLEALTDMEVANSIMKDARNTDTVHPLDRQFQGL
 NMQEMTPLEHTSTEFIELANYLNQ
 SRGHTGVQYKVINIFRIERQGEKDRFQSSMYSN
 IQNSCRRLLWHGSRSTNFGGILSQ
 GLRIAPPEAPVSGYMFVGKGVYFADMSTKSAGYCF
 SWGSGNRGLLLLCDVEVGNNPMYER
 DTASFNAGQEAKAEAKIATLGRGRSIPGGWKDAG
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intron 43853..43911

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/EC-number="3.5.1.11"
 /note="unnamed protein product;
 Function: penicillin V
 amidohydrolase (PVA) from F.
 oxysporum is used for the
 enzymatic hydrolysis of penicillin
 V (phenoxy-methylpenicillin) to
 6-aminopenicillanic acid (6-APA).
 6-APA is the active beta-lactam
 nucleus used in the manufacture of
 semi-synthetic penicillins.
 Similarity: the predicted A. niger
 protein shows strong similarity to
 the protein sequence penicillin V
 amidohydrolase (PVA) of patent
 US5516679-A from F. oxysporum (AC#
 AAW00291). Title: strong
 similarity to penicillin V
 amidohydrolase PVA from patent
 US5516679-A - Fusarium oxysporum
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 GGRQGYFAAAKYPNLF DGVLGAP
 ALNFPRLIGYMFVPPVHMFHSAAPPQCVFDTFWK
 AIIDECPLDGATDGLISDYNPQS
 CPFKPETLVGHTVTCPEMGSDSPVTITAQHATLV
 KQILQGPDLQDHPDLWTGLPPGAS
 FRGTANTQVINGSIVRPVPPFPIIGWIKNFVYRD
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		/number=2
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)	
		/locus-tag="An18e01190"
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gene	<49850...>51919	/locus-tag="An18g01200"
mRNA	join(<49850..49888, 49981..50173, 50233..50362, 50419..50614, 50702..50828, 50883..51127, 51199..51470, 51538...>51919)	/locus-tag="An18g01200"
CDS	join(49850..49888, 49981..50173, 50233..50362, 50419..50614, 50702..50828, 50883..51127, 51199..51470, 51538..51919)	/locus-tag="An18g01200"
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		/inference="profile:PFAM:PF00067"
		/inference="similar to AA sequence:UniProtKB:AFU81806.1"
		/note="unnamed protein product; Function: ord1 of A. flavus converts O-methylsterigmatocystin to aflatoxin B1. Pathway: ord1 of A. flavus catalyzes the last step of the aflatoxin biosynthetic pathway. Remark: aflatoxins comprise a group of polyketide-derived carcinogenic mycotoxins. Similarity: the predicted A. niger protein shows strong similarity to O-methylsterigmatocystin (OMST)-oxidoreductase (ord1) from A. flavus, which belongs to the CYP64 family of cytochrome P450-type monooxygenases. Title: strong similarity to O-methylsterigmatocystin oxidoreductase ord1 - Aspergillus flavus"

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52984..53309,
53368..53720))

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Function: SRPK2 from M. musculus
phosphorylates SF2/ASF, a member
of SR splicing factors. Remark:
overexpression of murine SRPK2
causes disassembly of
cotransfected SF2/ASF and
endogenous SC35. SRPK family
members may regulate the
disassembly of the SR proteins in
a tissue-specific manner.
Similarity: the predicted A. niger
protein shows similarity to SRPK2
from M. musculus and strong
similarity to putative
serine/threonine protein kinases
from several eucaryotic organisms.
Title: similarity to
SR-protein-specific kinase SRPK2 -
Mus musculus nucleus"
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LGYGVTSTVWLGRDLRDSKYVVLKIYVTGQEKNH
ELEIYNRMNAVEVEHPGRDLVRRLL
FDHFTVTGPHGPHVCLVHEPMGMSADTLLQKYIP
GNTMTLDEMKTTCIRQLLIALDFLH
SAARIVHTGKDLQLKNLLLPVPNTKTLETLEERE
VNDPSPRKILKDRTIYLSTVYNPG
GSGPLPLISDFGEARFGDVEKRDDIMPNNMYRAPEV
VLKENWNYKVDIWNVAMVAWDIVI
PRHMF DGRNADGIFDDR VHIAEMIALMGPPPASF
RERCRLAYVFWDEQGNWKDLAPIP
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gene	complement(<54105..>557 62)	/number=5 /locus-tag="An18g01220"
mRNA	complement(join(<54105. .54731,54787..55334, 55392..55500, 55559..>55762))	/locus-tag="An18g01220"
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 sequence:PIR:S64826"
 /note="unnamed protein product;
 Function: in *S. cerevisiae*,
 mutants (dal5) that lack
 allantoate transport have been
 isolated. these strains also
 exhibit a 60% loss of allantoate
 transport capability. Regulation:
 in *S. cerevisiae* Dal5 appears to
 be sensitive to nitrogen
 catabolite repression, feedback
 inhibition, and trans-inhibition.
 Regulation: in *S. cerevisiae*
 allantoate uptake is constitutive.
 Similarity: the predicted *A. niger*
 protein shows strong similarity to
 allantoate permease gene (DAL5)
 from *S. cerevisiae*, which belongs
 to the major facilitator
 superfamily. Title: strong
 similarity to allantoate permease
 Dal5 - *Saccharomyces cerevisiae*"
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 PNIYCLQKVPAAKWLGVNVALWGVAASAGAKN
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CDS       join(56384..56645, /locus-tag="An18g01230"
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57069..57368,
57430..57711,
57897..58158,
58326..58444)

                                /note="unnamed protein product;
                                Function: M. grisea Pth11 is a
                                pathogenicity gene. Function: M.
                                grisea Pth11p likely is involved
                                in host surface recognition.
                                Function: M. grisea pth11 mutants
                                of strain 4091-5-8 are
                                nonpathogenic due to a defect in
                                appressorium differentiation.
                                Localization: in M. grisea, a
                                Pth11-green fluorescent protein
                                fusion localised to the cell
                                membrane and vacuoles. Similarity:
                                similarity of the predicted A.
                                niger protein and M. grisea Pth11
                                is limited to the N-terminal half
                                of the protein sequences. Title:
                                similarity to integral membrane
                                protein PTH11 - Magnaporthe grisea
                                plasma membrane"
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stutzeri catalyzes the conversion
 salicylate + NADH + O(2) <=>
 catechol + NAD(+) + H(2)O + CO(2).
 Pathway: NahW of P. stutzeri is
 involved in the metabolization of
 naphthalene and salicylates (lower
 naphthalene degradation pathway).
 Similarity: the predicted A. niger
 protein shows similarity to
 salicylate hydroxylase (nahW) of
 P. stutzeri, which belongs to the
 NADH-dependent monooxygenase
 superfamily. Title: similarity to
 salicylate hydroxylase nahW
 -Pseudomonas stutzeri"
 /citation=

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sequence:PIR:S45605"

/note="unnamed protein product;
 Catalytic activity: alcohol + NAD+
 = aldehyde or ketone + NADH.
 Pathway: alcohol dehydrogenase
 ADH-T from B. stearothermophilus
 is involved in glycolysis /
 gluconeogenesis; fatty acid
 metabolism; bile acid
 biosynthesis; tyrosine metabolism;
 glycerolipid metabolism. Remark:
 the protein sequence of alcohol
 dehydrogenase ADH-T from B.
 stearothermophilus NCA1503 is
 covered by patent JP04218378-A
 (AC# AAR26874). Similarity: the
 predicted A. niger protein shows
 strong similarity to thermostable
 alcohol dehydrogenase ADH-T from
 B. stearothermophilus NCA1503,
 which belongs to the zinc alcohol
 dehydrogenase (ADH) family. Title:
 strong similarity to thermostable
 alcohol dehydrogenase adhT -
 Bacillus stearothermophilus"
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exon

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mRNA	join(<101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..>104542)	/locus-tag="An18g01440"
CDS	join(101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..104542)	/locus-tag="An18g01440"
		/inference="profile:COGS:COG3496" /note="unnamed protein product; Similarity: the predicted A. niger protein shows local similarity to the hypothetical protein mll8086 from M. loti. Title: strong similarity to hypothetical protein CAD70872.1 - Neurospora crassa" /codon-start=1 /protein-id="CAK47217.1" /db-xref="GI:134084184" /translation="MTAKCMVIKKAEDHTEFLG LHHVGSCKNFDNCVTKEVRGPQIL KKFLLRQWIPAQGGREQQPESLILSPVRKNLPSI SVDGILLHAALLTVNLILKLGGWP GLLKFMLRFTAISSVLAPIGLIGFLVLSFTPRN IKSLSKDKSVIGKPLLPITLDHT RLSPIKNNFTFNVLFVVGIPVGISCRFGRLLSIDA KHTDEEECTERSLLRLLQTYFSS WFSFDSARYLHRGDDTLSLENKLNKFLREQNENP AKWPYAYMLSVPRFLWWERSVVTW WYLYSESKELDAVIMEINNSFDEKRNVLFKVVRT RIYTESPEKGFEQLLDCKEEHLDE DKRVFSLIPQHGYAYKATWKKEIFSSPFKVGGE TVSSTFLDPVVPSSWSGNRSLNNT TTFDPSPGAPRMARLWCKVPPIDPGKASSFQIFS ILLIWTNVNLTATPRILFQAIRLH VMNLMRMMEHPDVRPGSEPRRPSKGERKDAPLKM LHSFLDLHANLQSRMLERFFREYL KHIVASYPGDLEVITYIPCKSVFKTTICLRSTQYS AEGQDPRLRLLEVMDPAFYSRIVN SPNAGTAMAKETKGRSPADALSSPVIASDITQS LQLLDVTVSENRTYDKACSRISW VLCLRRWLTSSFMDSFVCKALPPRTQEEYVSCLI QLWLEKLTWDFLSPHQIYRVIRAA MLQWAICWILF"
exon	101875..101958	/locus-tag="An18g01440"
intron	101959..102202	/number=1 /locus-tag="An18g01440"
exon	102203..102219	/number=1 /locus-tag="An18g01440"
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intron	102361..102391	/locus-tag="An18g01440"
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exon	102392..102399	/locus-tag="An18g01440"
		/number=4
intron	102400..102620	/locus-tag="An18g01440"
		/number=4
exon	102621..103153	/locus-tag="An18g01440"
		/number=5
intron	103154..103204	/locus-tag="An18g01440"
		/number=5
exon	103205..104542	/locus-tag="An18g01440"
		/number=6
gene	<106231..>106803	/locus-tag="An18g01450"
mRNA	join(<106231..106565, 106647..>106803)	/locus-tag="An18g01450"
CDS	join(106231..106565, 106647..106803)	/locus-tag="An18g01450"
		/EC-number="1.14.-.-"
		/note="unnamed protein product; Function: ordA of A. parasiticus is involved in the aflatoxin biosynthesis and converts O-methylsterigmatocystin (OMST) to aflatoxins B1 or G1 and converts dihydro-O-methylsterigmatocystin (DHOMST) to aflatoxins B2 or G2. Remark: aflatoxins comprise a group of polyketide-derived carcinogenic mycotoxins. Remark: it is assumed that the ORF is N-terminally shorter and has another start codon 5' to the predicted one ; the ORF is around 400 amino acids shorter than most of the homologues cytochrome p450 proteins. Remark: ordA of A. parasiticus is also called cytochrome p450 64, cyp64 or omst oxidoreductase. Similarity: the ORF shows similarity to several cytochrome P450 related proteins from different species. Title: strong similarity to O-methylsterigmatocystin oxidoreductase ordA - Aspergillus parasiticus"
		/citation=[43]
		/codon-start=1
		/protein-id="CAK47218.1"
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		/translation="MTFNPERFLTTESYQAEHDP HNLAFGFGRRICPGRGFADSTIFL TVVRSLQAFRIAKISEDGREIEPIVEYLPGVISH PKPFAISITPRSKEHESFIRSIEI EHPWEKGDLVSILSVNLVVVASKLRVFTILTSL YRLPLIGNCKPPNLLLGRMGLIRF SLH"
exon	106231..106565	/locus-tag="An18g01450"
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intron	106566..106646	/locus-tag="An18g01450"
		/number=1
exon	106647..106803	/locus-tag="An18g01450"
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gene	<107279..>108340	/locus-tag="An18g01460"
mRNA	join(<107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..>108340)	/locus-tag="An18g01460"
CDS	join(107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..108340)	/locus-tag="An18g01460"
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		/inference="profile:COGS:COG1028"
		/inference="profile:PFAM:PF00106"
		/note="unnamed protein product; Catalytic activity: cyclohexanol dehydrogenases convert cyclohexanol + NAD(+) <=> cyclohexanone + NADH. Function: chnA of A. sp. is an alcohol dehydrogenases proposed to catalyze the conversion of cyclohexanol to cyclohexanone (EC 1. 1. 1. 245). Phenotype: cyclohexanol was detected as the major intermediate accumulated in the chnA mutant of A. sp. Remark: chnA of A. sp. is encoded in the gene cluster for cyclohexanol oxidation. Similarity: the ORF shows similarity to several dehydrogenases from different species and with various specificities. Title: strong similarity to cyclohexanol dehydrogenase chnA - Acinetobacter sp"
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sig-peptide	join(107279..107327, 107380..107387)	/locus-tag="An18g01460"
		/inference="protein motif:SignalP:2.0"
mat-peptide	join(107388..107740,	/locus-tag="An18g01460"

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intron	107741..107794	/locus-tag="An18g01460" /number=2
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intron	107908..107965	/locus-tag="An18g01460" /number=3
exon	107966..107988	/locus-tag="An18g01460" /number=4
intron	107989..108044	/locus-tag="An18g01460" /number=4
exon	108045..108097	/locus-tag="An18g01460" /number=5
intron	108098..108150	/locus-tag="An18g01460" /number=5
exon	108151..108340	/locus-tag="An18g01460" /number=6
gene	<108826..>111209	/locus-tag="An18g01470"
mRNA	join(<108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960, 111135..>111209)	/locus-tag="An18g01470"
CDS	join(108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960, 111135..111209)	/locus-tag="An18g01470"
		/EC-number="1.14.-.-" /inference="profile:COGS:COG0493" /note="unnamed protein product; Remark: aflatoxins are polyketide-derived secondary metabolites. Remark: moxY of A. parasiticus is expressed concurrently with genes involved in aflatoxin biosynthesis and it lies on one end of the cluster of this genes. Therefore moxY of A. parasiticus is presumably also

involved in aflatoxin biosynthesis. Similarity: the ORF shows similarity to monooxygenases from several species and with different functions. Title: strong similarity to monooxygenase moxY -*Aspergillus parasiticus* "/>

exon 108826..108944
intron 108945..109019
exon 109020..109023
intron 109024..109088
exon 109089..109305
intron 109306..109376
exon 109377..109778
intron 109779..109840
exon 109841..109905
intron 109906..110159
exon 110160..110181
intron 110182..110243
exon 110244..110293
intron 110294..110354
exon 110355..110492
intron 110493..110523
exon 110524..110752

intron	110753..110865	/locus-tag="An18g01470"
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intron	110961..111134	/locus-tag="An18g01470"
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exon	111135..111209	/locus-tag="An18g01470"
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gene	<111907..>113460	/locus-tag="An18g01480"
mRNA	<111907..>113460	/locus-tag="An18g01480"
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		/inference="profile:PFAM:PF00067"
		/inference="similar to AA
		sequence:UniProtKB:AB013443.1"
		/note="unnamed protein product;
		Function: eln2 of C. cinereus
		encodes a novel type of microsomal
		cytochrome P450 enzyme, with is
		involved in mushroom
		morphogenesis. Phenotype: a
		dominant mutation of the
		elongationless2 (eln2) gene of the
		mushroom C. cinereus affects
		pattern formation in the
		development of fruit body
		primordia, causing dumpy primordia
		which culminate in mature fruit
		bodies with short stipes.
		Similarity: the ORF shows
		similarity to several cytochrome
		p450 related proteins from
		different species, which have
		different cellular functions.
		Title: strong similarity to
		cytochrome p450 related protein
		eln2 - Coprinus cinereus"
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		ITKGLHMLIRQYDDWLRHLHQRLDAPLLSPRASNT
		YHPIQDLESKQLMFDLLRSNDFDA
		HFERYSGSLMFALAYGFRLLSPKGQELRDMRTIQ
		GNFTYAARVGTWIVDAIPVLNLYLP
		AVVAPWKRLAEKLFKLEASVHTRHLEKGLNSEPW
		NWSKEFAASKHAEGMPRLDLAYNL
		GILVDAGFETTWTVMKIFVLAMRSDPRFVAVARK
		ELDEVVGEDRMPTFEDQEKLVIYIQ
		AVVDETLRWRSMA PGGIPHAARKEDTYMGYRIPK
		GATVIPLFWSMCLTDEPWDDPLEF
		RPERWFEATEKEEGRFRNFFGYGRRICTGRHIAR
		NSLFLLMARILWAFDIQAPLGDDG
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sig-peptide	111907..111957	/locus-tag="An18g01480"
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mat-peptide	111958..113457	motif:SignalP:2.0" /locus-tag="An18g01480" /product="unnamed"
exon	111907..113460	/locus-tag="An18g01480" /number=1
gene	complement(<113565..>114733)	/locus-tag="An18g01490"
mRNA	complement(join(<113565..114153, 114210..>114733))	/locus-tag="An18g01490"
CDS	complement(join(113565..114153, 114210..114733))	/locus-tag="An18g01490" /inference="profile:COGS:COG0598" /inference="profile:PFAM:PF01544" /inference="similar to AA sequence:UniProtKB:SC41293.1" /note="unnamed protein product; Function: alr2 of S. cerevisiae is an uptake transporter for inorganic cations, e. g. magnesium, which presence seems to be important for resistance to the toxic effect of aluminum. Remark: alr2 of S. cerevisiae is also called YFL050C. Similarity: the predicted ORF is 395 amino acids shorter at the N-terminus and 57 amino acids shorter at its C-terminal end than alr2 of S. cerevisiae (nearly the same is true for alr1 of S. cerevisiae). Title: strong similarity to ion transporter Alr2 -Saccharomyces cerevisiae plasma membrane" /citation=[40] /codon-start=1 /protein-id="CAK47222.1" /db-xref="GI:134084189" /translation="MSSDSTPDPRLEKPRVAVAS RLNFFTSQLNTSIEASSIEDLCSV YRPFELLLETGAHSGLWLDITAPSEEDIEALAR FFNLHPLTTEDIKTRETREKIELF GQYYFLSLRPPRRLETDGTGVRIVSHNLYAVVFRG GVLSFSFDPSLHTSHVRQRIEHS SHLLLTSDWICYALIDDIVDGFAPFISRVENGVV TVEDSVSITRPDDMGLALQRIFKL RKEVMNIRQPLHDKIDVIRSFARHCDISDTSSSQ VALYLSDICDHVVTMIANLEQAEQ MLSRLQSKYLTQVHFDSGRMRNGIASALSKLTVL ASILVPMQFITGLFGMNVVRPGKT HDGDNSTLWWFSILGFILGLTVIFAWVAKRIGLL DR"
exon	complement(113565..114153)	/locus-tag="An18g01490" /number=1
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AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
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SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELL? AND
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0* FILE NUTRACEUT
1* FILE PASCAL
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L5 ANSWER 1 OF 27 USPATFULL on STN
AN 2007:296111 USPATFULL
TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface
```

protein homologues and uses therefore

IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
 Altermann, Eric, Palmerston North, NEW ZEALAND
 Buck, B. Logan, Banner Elk, NC, UNITED STATES
 Russell, W. Michael, Newburgh, IN, UNITED STATES

PA North Carolina State University, Raleigh, NC, UNITED STATES (U.S. corporation)

PI US 20070258955 A1 20071108

AI US 2007-701335 A1 20070201 (11)

RLI Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING

PRAI US 2003-465621P 20030425 (60)

DT Utility

FS APPLICATION

LN.CNT 5104

INCL INCLM: 424/093.400
 INCLS: 435/252.100; 435/252.900; 435/320.100; 435/006.000; 435/007.100;
 435/070.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100

NCL NCLM: 424/093.400
 NCLS: 435/006.000; 435/007.100; 435/070.100; 435/252.100; 435/252.900;
 435/320.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100

IC IPCI A61K0035-00 [I,A]; A61K0038-00 [I,A]; A61P0001-00 [I,A];
 C07H0021-02 [I,A]; C07H0021-00 [I,C*]; C07K0016-00 [I,A];
 C07K0004-00 [I,A]; C12N0001-20 [I,A]; C12N0015-00 [I,A];
 C12P0021-04 [I,A]; C12Q0001-68 [I,A]

IPCR A61K0035-00 [I,C]; A61K0035-00 [I,A]; A61K0038-00 [I,C];
 A61K0038-00 [I,A]; A61P0001-00 [I,C]; A61P0001-00 [I,A];
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 C07K0014-335 [I,A]; C07K0016-00 [I,C]; C07K0016-00 [I,A];
 C12N0001-20 [I,C]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
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 C12P0021-04 [I,A]; C12P0021-06 [I,C*]; C12P0021-06 [I,A];
 C12Q0001-68 [I,C]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 2

L5 ANSWER 2 OF 27 USPATFULL on STN

AN 2007:197155 USPATFULL

TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface protein homologues and uses therefore

IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
 Altermann, Eric, Palmerston North, NEW ZEALAND
 Buck, B. Logan, Banner Elk, NC, UNITED STATES
 Russell, W. Michael, Newburgh, IN, UNITED STATES

PA North Carolina State University, Raleigh, NC, UNITED STATES, 27695-8210 (U.S. corporation)

PI US 20070172495 A1 20070726

AI US 2007-701319 A1 20070201 (11)

RLI Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING

PRAI US 2003-465621P 20030425 (60)

DT Utility

FS APPLICATION

LN.CNT 5104

INCL INCLM: 424/234.100
 INCLS: 514/044.000; 435/006.000; 435/007.320; 435/069.100; 435/252.900;
 435/471.000; 530/350.000; 536/023.700

NCL NCLM: 424/234.100
 NCLS: 435/006.000; 435/007.320; 435/069.100; 435/252.900; 435/471.000;
 514/044.000; 530/350.000; 536/023.700

IC IPCI A61K0048-00 [I,A]; A61K0039-02 [I,A]; C12Q0001-68 [I,A];
G01N0033-554 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*];
C12P0021-06 [I,A]; C07K0014-335 [I,A]; C07K0014-195 [I,C*];
IPCR A61K0048-00 [I,C]; A61K0048-00 [I,A]; A61K0039-02 [I,C];
A61K0039-02 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];
C07K0014-195 [I,C]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
C12P0021-06 [I,C]; C12P0021-06 [I,A]; C12Q0001-68 [I,C];
C12Q0001-68 [I,A]; G01N0033-554 [I,C]; G01N0033-554 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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L5 ANSWER 3 OF 27 USPATFULL on STN
AN 2007:140436 USPATFULL
TI Delivery of trefoil peptides
IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
Steidler, Lothar, Lokeren, BELGIUM
Remaut, Erik Rene, Lovendegem, BELGIUM
PI US 20070122427 A1 20070531
AI US 2007-654879 A1 20070118 (11)
RLI Division of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A 371
of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000
PRAI EP 1999-870143 19990705
DT Utility
FS APPLICATION
LN.CNT 1335
INCL INCLM: 424/200.100
INCLS: 435/252.300; 435/252.900
NCL NCLM: 424/200.100
NCLS: 435/252.300; 435/252.900
IC IPCI A61K0039-02 [I,A]; C12N0001-21 [I,A]
IPCR A61K0039-02 [I,C]; A61K0039-02 [I,A]; C12N0001-21 [I,C];
C12N0001-21 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 4

L5 ANSWER 4 OF 27 USPATFULL on STN
AN 2007:134502 USPATFULL
TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
(non-U.S. corporation)
PI US 20070117183 A1 20070524
AI US 2006-511140 A1 20060828 (11)
RLI Division of Ser. No. US 2005-55822, filed on 11 Feb 2005, PENDING
Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
PRAI DE 1999-19932125 19990709
DE 1999-19932227 19990709
DE 1999-19932228 19990709
DE 1999-19932230 19990709
DE 1999-19933005 19990714
DE 1999-19933006 19990714
DE 1999-19940764 19990827
DE 1999-19940766 19990827

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DE	1999-19931453	19990708
DE	1999-19931457	19990708
DE	1999-19931465	19990708
DE	1999-19931478	19990708
DE	1999-19931510	19990708
DE	1999-19931541	19990708
DE	1999-19931573	19990708
DE	1999-19931592	19990708
DE	1999-19931632	19990708
DE	1999-19931634	19990708
DE	1999-19931636	19990708
DE	1999-19932130	19990709
DE	1999-19932186	19990709
DE	1999-19932922	19990714
DE	1999-19932926	19990714
DE	1999-19933004	19990714
DE	1999-19940765	19990827
DE	1999-19941380	19990831
DE	1999-19941394	19990831
DE	1999-19942076	19990903
DE	1999-19942086	19990903
DE	1999-19942095	19990903
DE	1999-19942129	19990903
US	1999-141031P	19990625 (60)
US	1999-142101P	19990702 (60)
US	1999-148613P	19990812 (60)
US	2000-187970P	20000309 (60)

DT Utility
FS APPLICATION

LN.CNT 8386

INCL INCL: 435/069.100
INCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
536/023.200

NCL NCLM: 435/069.100
NCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
536/023.200

IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12P0021-06 [I,A];
C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
C12N0009-10 [I,A]; C12N0015-74 [I,A]; C12N0001-21 [I,A]

IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C];
C12N0001-21 [I,A]; C12N0009-10 [I,C]; C12N0009-10 [I,A];
C12N0015-74 [I,C]; C12N0015-74 [I,A]; C12P0013-00 [I,C];
C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0021-06 [I,C];
C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 6

L5 ANSWER 6 OF 27 USPATFULL on STN
AN 2007:130427 USPATFULL
TI Delivery of trefoil peptides
IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
Steidler, Lothar, Lokeren, BELGIUM
Remaut, Erik Rene, Lonendegem, BELGIUM
PA Vlaams Interuniversitair Instituut voor Biotechnologie, BELGIUM
(non-U.S. corporation)
PI US 7220418 B1 20070522
WO 2001002570 20010111
AI US 2000-30390 20000705 (10)
WO 2000-EP6343 20000705
20020416 PCT 371 date
PRAI EP 1999-870143 19990705
DT Utility
FS GRANTED
LN.CNT 1334
INCL INCLM: 424/200.100
INCLS: 424/093.450; 424/093.200; 424/234.100; 424/192.100; 514/925.000
NCL NCLM: 424/200.100
NCLS: 424/093.200; 424/093.450; 424/192.100; 424/234.100; 514/925.000
IC IPCI A01N0063-00 [I,A]; A61K0039-02 [I,A]; A61K0039-00 [I,A]
IPCR A01N0063-00 [I,C]; A01N0063-00 [I,A]; C12N0015-09 [I,C*];
C12N0015-09 [I,A]; A61K0035-66 [I,C*]; A61K0035-74 [I,A];
A61K0038-00 [I,C*]; A61K0038-00 [I,A]; A61K0039-00 [I,C];
A61K0039-00 [I,A]; A61K0039-02 [I,C]; A61K0039-02 [I,A];
A61K0048-00 [I,C*]; A61K0048-00 [I,A]; A61P0001-00 [I,C*];
A61P0001-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-575 [I,A];
C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0015-16 [I,C*];
C12N0015-16 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
C12R0001-01 [N,A]
EXF 424/200.1; 424/192.1; 424/184.1; 424/234.1; 424/244.1; 424/246.1;
424/93.2; 424/93.45; 514/2; 514/925; 435/69.3; 435/69.1; 435/71.1;
435/252.9

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 7

L5 ANSWER 7 OF 27 IFIPAT COPYRIGHT 2008 IFI on STN
AN 11053905 IFIPAT;IFIUDB;IFICDB
TI METHOD OF IMPROVING IMMUNE FUNCTION IN MAMALS USING LACTOBACILLUS
REUTERI STRAINS
IN Kang Ho-Jin (KR); Kwon Ik-boo (KR); Lee Dong-Seog (KR); Mollstam Bo (SE)
PA Unassigned Or Assigned To Individual (68000)
PI US 2006002907 A1 20060105
AI US 2002-531651 20021018
WO 2002-SE1903 20021018
20050415 PCT 371 date
20050415 PCT 102(e) date
FI US 2006002907 20060105
DT Utility; Patent Application - First Publication

FS CHEMICAL
 APPLICATION
ED Entered STN: 9 Jan 2006
 Last Updated on STN: 9 Jan 2006
CLMN 9
GI 1 Figure(s).
FIG. 1. Confirmation of inhibitory ability against the binding of vero
cytotoxin(VT) and Gb3 receptor in a culture supernatant of L. reuteri
through competitive ELISA. Each reacted as follows, on plates coated with
Gb3, followed by performing ELISA using mAb against VT.

=> d 15 8

L5 ANSWER 8 OF 27 USPATFULL on STN
AN 2006:274450 USPATFULL
TI Gene products differentially expressed in cancerous cells
IN Scott, Elizabeth M., Emeryville, CA, UNITED STATES
 Lamson, George, Emeryville, CA, UNITED STATES
 Kassam, Altaf, Emeryville, CA, UNITED STATES
 Zhang, Guozhong, Emeryville, CA, UNITED STATES
 Sakamoto, Doreen, Emeryville, CA, UNITED STATES
 Garcia, Pablo Dominguez, Emeryville, CA, UNITED STATES
 May, Theresa, Emeryville, CA, UNITED STATES
 Kennedy, Giulia C., Emeryville, CA, UNITED STATES
 Kang, Sanmao, Emeryville, CA, UNITED STATES
 Reinhard, Christoph, Emeryville, CA, UNITED STATES
 Jefferson, Ann Bennett, Emeryville, CA, UNITED STATES
PA Chiron Corporation (U.S. corporation)
PI US 20060234246 A1 20061019
AI US 2004-934842 A1 20040902 (10)
RLI Continuation-in-part of Ser. No. US 2002-165835, filed on 6 Jun 2002,
 ABANDONED Continuation of Ser. No. US 2000-490818, filed on 25 Jan 2000,
 GRANTED, Pat. No. US 6429302 Continuation-in-part of Ser. No. US
 2001-883152, filed on 15 Jun 2001, ABANDONED Continuation-in-part of
 Ser. No. WO 2003-US15465, filed on 16 May 2003, PENDING
PRAI US 1999-118302P 19990202 (60)
 US 2000-211835P 20000615 (60)
 US 2003-445222P 20030204 (60)
 US 2002-381533P 20020517 (60)
DT Utility
FS APPLICATION
LN.CNT 17024
INCL INCLM: 435/006.000
 INCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
 530/388.800; 536/023.500
NCL NCLM: 435/006.000
 NCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
 530/388.800; 536/023.500
IC IPCI C12Q0001-68 [I,A]; G01N0033-574 [I,A]; C07H0021-04 [I,A];
 C07H0021-00 [I,C*]; C12P0021-06 [I,A]; C07K0014-82 [I,A];
 C07K0016-30 [I,A]; C07K0016-18 [I,C*]
 IPCR C12Q0001-68 [I,C]; C12Q0001-68 [I,A]; C07H0021-00 [I,C];
 C07H0021-04 [I,A]; C07K0014-82 [I,C]; C07K0014-82 [I,A];
 C07K0016-18 [I,C]; C07K0016-30 [I,A]; C12P0021-06 [I,C];
 C12P0021-06 [I,A]; G01N0033-574 [I,C]; G01N0033-574 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 9

L5 ANSWER 9 OF 27 USPATFULL on STN

AN 2006:98984 USPATFULL
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
 (non-U.S. corporation)
 PI US 20060084152 A1 20060420
 AI US 2005-239674 A1 20050928 (11)
 RLI Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED
 Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
 ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23
 Jun 2000, ABANDONED
 PRAI DE 1999-19932125 19990709
 DE 1999-19932227 19990709
 DE 1999-19932228 19990709
 DE 1999-19932230 19990709
 DE 1999-19933005 19990714
 DE 1999-19933006 19990714
 DE 1999-19940764 19990827
 DE 1999-19940766 19990827
 DE 1999-19940832 19990827
 DE 1999-19941378 19990831
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 DE 1999-19941396 19990831
 DE 1999-19942087 19990903
 DE 1999-19930476 19990701
 DE 1999-19931419 19990708
 DE 1999-19931420 19990708
 DE 1999-19932206 19990709
 DE 1999-19942088 19990903
 DE 1999-19942124 19990903
 DE 1999-19932928 19990714
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 DE 1999-19931478 19990708
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 DE 1999-19931634 19990708
 DE 1999-19931636 19990708
 DE 1999-19932130 19990708
 DE 1999-19932186 19990709
 DE 1999-19932922 19990714
 DE 1999-19932926 19990714
 DE 1999-19933004 19990714

DE	1999-19940765	19990827
DE	1999-19941380	19990831
DE	1999-19941394	19990831
DE	1999-19942076	19990903
DE	1999-19942086	19990903
DE	1999-19942095	19990903
DE	1999-19942129	19990903
DE	1999-19932124	19990709
DE	1999-19932127	19990709
DE	1999-19932133	19990709
DE	1999-19932207	19990709
DE	1999-19932208	19990709
DE	1999-19932225	19990709
DE	1999-19932914	19990709
DE	1999-19940768	19990827
DE	1999-19940831	19990827
DE	1999-19941385	19990831
US	1999-141031P	19990625 (60)
US	1999-142101P	19990702 (60)
US	1999-148613P	19990812 (60)
US	2000-187970P	20000309 (60)
US	1999-141031P	19990625 (60)
US	1999-143694P	19990714 (60)
US	1999-151778P	19990831 (60)
DT	Utility	
FS	APPLICATION	
LN.CNT	14822	
INCL	INCLM: 435/113.000	
	INCLS: 435/115.000; 435/252.300	
NCL	NCLM: 435/113.000	
	NCLS: 435/115.000; 435/252.300	
IC	IPCI C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];	
	C12N0001-20 [I,A]	
	IPCR C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];	
	C12N0001-20 [I,A]; C12P0013-08 [I,A]	
CAS INDEXING IS AVAILABLE FOR THIS PATENT.		

=> d 15 9

L5 ANSWER 9 OF 27 USPATFULL on STN

AN 2006:98984 USPATFULL

TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
(non-U.S. corporation)

PI US 20060084152 A1 20060420

AI US 2005-239674 A1 20050928 (11)

RLI Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED
Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23
Jun 2000, ABANDONED

PRAI DE 1999-19932125 19990709
DE 1999-19932227 19990709
DE 1999-19932228 19990709
DE 1999-19932230 19990709
DE 1999-19933005 19990714
DE 1999-19933006 19990714

DE 1999-19940764	19990827
DE 1999-19940766	19990827
DE 1999-19940832	19990827
DE 1999-19941378	19990831
DE 1999-19941379	19990831
DE 1999-19942077	19990903
DE 1999-19942079	19990903
DE 1999-19931418	19990708
DE 1999-19932126	19990709
DE 1999-19932229	19990709
DE 1999-19941396	19990831
DE 1999-19942087	19990903
DE 1999-19930476	19990701
DE 1999-19931419	19990708
DE 1999-19931420	19990708
DE 1999-19932206	19990709
DE 1999-19942088	19990903
DE 1999-19942124	19990903
DE 1999-19932928	19990714
DE 1999-19931415	19990708
DE 1999-19931424	19990708
DE 1999-19931428	19990708
DE 1999-19931434	19990708
DE 1999-19931435	19990708
DE 1999-19931443	19990708
DE 1999-19931453	19990708
DE 1999-19931457	19990708
DE 1999-19931465	19990708
DE 1999-19931478	19990708
DE 1999-19931510	19990708
DE 1999-19931541	19990708
DE 1999-19931573	19990708
DE 1999-19931592	19990708
DE 1999-19931632	19990708
DE 1999-19931634	19990708
DE 1999-19931636	19990708
DE 1999-19932130	19990708
DE 1999-19932186	19990709
DE 1999-19932922	19990714
DE 1999-19932926	19990714
DE 1999-19933004	19990714
DE 1999-19940765	19990827
DE 1999-19941380	19990831
DE 1999-19941394	19990831
DE 1999-19942076	19990903
DE 1999-19942086	19990903
DE 1999-19942095	19990903
DE 1999-19942129	19990903
DE 1999-19932124	19990709
DE 1999-19932127	19990709
DE 1999-19932133	19990709
DE 1999-19932207	19990709
DE 1999-19932208	19990709
DE 1999-19932225	19990709
DE 1999-19932914	19990709
DE 1999-19940768	19990827
DE 1999-19940831	19990827
DE 1999-19941385	19990831
US 1999-141031P	19990625 (60)
US 1999-142101P	19990702 (60)
US 1999-148613P	19990812 (60)
US 2000-187970P	20000309 (60)

US 1999-141031P 19990625 (60)
 US 1999-143694P 19990714 (60)
 US 1999-151778P 19990831 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 14822
 INCL INCLM: 435/113.000
 INCLS: 435/115.000; 435/252.300
 NCL NCLM: 435/113.000
 NCLS: 435/115.000; 435/252.300
 IC IPCI C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
 C12N0001-20 [I,A]
 IPCR C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];
 C12N0001-20 [I,A]; C12P0013-08 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 10

L5 ANSWER 10 OF 27 USPATFULL on STN
 AN 2006:211028 USPATFULL
 TI Nucleic acid sequences relating to Bacteroides fragilis for diagnostics
 and therapeutics
 IN Breton, Gary L., Marlboro, MA, UNITED STATES
 PA Oscient Pharmaceuticals Corporation, Waltham, MA, UNITED STATES (U.S.
 corporation)
 PI US 7090973 B1 20060815
 AI US 2000-540209 20000404 (9)
 PRAI US 1999-128705P 19990409 (60)
 DT Utility
 FS GRANTED
 LN.CNT 38850
 INCL INCLM: 435/006.000
 INCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
 NCL NCLM: 435/006.000
 NCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
 IC IPCI C12Q0001-68 [I,A]; C12P0019-34 [I,A]; C12P0019-00 [I,C*];
 C07H0021-02 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*]
 EXF 435/91.1; 435/91.2; 435/6; 435/320.1; 435/325; 435/352.3; 536/23.1;
 536/24.1; 536/23.7; 536/24.32; 536/24.3; 514/44
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 11-15

L5 ANSWER 11 OF 27 USPATFULL on STN
 AN 2006:146715 USPATFULL
 TI Nucleic acid and amino acid sequences relating to Staphylococcus
 epidermidis for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn, Framingham, MA, UNITED STATES
 Bush, David, Somerville, MA, UNITED STATES
 PA Wyeth, Madison, NJ, UNITED STATES (U.S. corporation)
 PI US 7060458 B1 20060613
 AI US 1999-450969 19991129 (9)
 RLI Continuation-in-part of Ser. No. US 1998-134001, filed on 13 Aug 1998,
 Pat. No. US 6380370, issued on 30 Apr 2002
 PRAI US 1997-64964P 19971108 (60)
 US 1997-55779P 19970814 (60)
 DT Utility
 FS GRANTED
 LN.CNT 35708
 INCL INCLM: 435/069.100

INCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
NCL NCLM: 435/069.100
NCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C*]
IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]
EXF 435/6; 435/91.2; 435/69.1; 536/22.1; 536/23.1; 536/24.3
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 12 OF 27 USPATFULL on STN
AN 2005:299042 USPATFULL
TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
(non-U.S. corporation)
PI US 20050260707 A1 20051124
AI US 2005-55822 A1 20050211 (11)
RLI Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
PRAI DE 1999-19932125 19990709
DE 1999-19932227 19990709
DE 1999-19932228 19990709
DE 1999-19932230 19990709
DE 1999-19933005 19990714
DE 1999-19933006 19990714
DE 1999-19940764 19990827
DE 1999-19940766 19990827
DE 1999-19940832 19990827
DE 1999-19941378 19990831
DE 1999-19941379 19990831
DE 1999-19942077 19990903
DE 1999-19942079 19990903
DE 1999-19931418 19990708
DE 1999-19932126 19990709
DE 1999-19932229 19990709
DE 1999-19941396 19990831
DE 1999-19942087 19990903
DE 1999-19930476 19990701
DE 1999-19931419 19990708
DE 1999-19931420 19990708
DE 1999-19932206 19990709
DE 1999-19942088 19990903
DE 1999-19942124 19990903
DE 1999-19932928 19990714
DE 1999-19931415 19990708
DE 1999-19931424 19990708
DE 1999-19931428 19990708
DE 1999-19931434 19990708
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DE 1999-19931478 19990708
DE 1999-19931510 19990708
DE 1999-109931541 19990708
DE 1999-19931573 19990708
DE 1999-19931592 19990708
DE 1999-19931632 19990708

DE 1999-19931634 19990708
 DE 1999-19931636 19990708
 DE 1999-19932130 19990708
 DE 1999-19932186 19990709
 DE 1999-19932922 19990714
 DE 1999-19932926 19990714
 DE 1999-19933004 19990714
 DE 1999-19940765 19990827
 DE 1999-19941380 19990831
 DE 1999-19941394 19990831
 DE 1999-19942076 19990903
 DE 1999-19942086 19990903
 DE 1999-19942095 19990903
 DE 1999-19942129 19990903
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 8777
 INCL INCLM: 435/069.100
 INCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200
 NCL NCLM: 435/069.100
 NCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200
 IC [7]
 ICM C12P021-06
 ICS C12P013-04; C07H021-04; C12N001-20; C12N015-74; C12N009-10
 IPCI C12P0021-06 [ICM,7]; C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*];
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]; C12N0001-20 [ICS,7];
 C12N0015-74 [ICS,7]; C12N0009-10 [ICS,7]
 IPCR C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
 C07K0014-34 [I,A]; C12N0001-20 [I,C*]; C12N0001-20 [I,A];
 C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
 C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
 C12P0013-00 [I,C*]; C12P0013-04 [I,A]; C12P0021-06 [I,C*];
 C12P0021-06 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 L5 ANSWER 13 OF 27 USPATFULL on STN
 AN 2005:268092 USPATFULL
 TI Modified bacterial surface layer proteins
 IN Pouwels, Pieter Hendrik, Rijswijk, NETHERLANDS
 Smit, Egbert, Sittard, NETHERLANDS
 Tielen, Frans, Prinsenbeek, NETHERLANDS
 PI US 20050233408 A1 20051020
 AI US 2003-500307 A1 20021223 (10)
 WO 2002-EP14749 20021223
 20041122 PCT 371 date
 PRAI EP 2001-310937 20011228
 DT Utility
 FS APPLICATION
 LN.CNT 2664
 INCL INCLM: 435/034.000
 INCLS: 530/395.000; 435/252.300
 NCL NCLM: 435/034.000
 NCLS: 435/252.300; 530/395.000
 IC [7]
 ICM C12Q001-04
 ICS C12N001-21; C07K014-335
 IPCI C12Q0001-04 [ICM,7]; C12N0001-21 [ICS,7]; C07K0014-335 [ICS,7];
 C07K0014-195 [ICS,7,C*]

IPCR C12N0015-09 [I,C*]; C12N0015-09 [I,A]; A61K0039-02 [I,C*];
A61K0039-02 [I,A]; A61P0031-00 [I,C*]; A61P0031-04 [I,A];
C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-15 [I,C*];
C12N0001-15 [I,A]; C12N0001-19 [I,C*]; C12N0001-19 [I,A];
C12N0001-20 [I,C*]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12N0005-10 [I,C*]; C12N0005-10 [I,A];
C12N0015-31 [I,C*]; C12N0015-31 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 14 OF 27 USPATFULL on STN

AN 2005:220997 USPATFULL

TI Corynebacterium glutamicum genes encoding proteins involved in
homeostasis and adaptation

IN Pompejus, Markus, Waldsee, GERMANY, FEDERAL REPUBLIC OF
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF

PA Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF,
D-67056 (non-U.S. corporation)

PI US 20050191732 A1 20050901

AI US 2003-721922 A1 20031124 (10)

RLI Continuation of Ser. No. US 2000-603124, filed on 23 Jun 2000, ABANDONED

PRAI DE 1999-19931418 19990708
DE 1999-19932124 19990709
DE 1999-19932126 19990709
DE 1999-19932127 19990709
DE 1999-19932133 19990709
DE 1999-19932207 19990709
DE 1999-19932208 19990709
DE 1999-19932225 19990709
DE 1999-19932229 19990709
DE 1999-19932914 19990709
DE 1999-19933006 19990709
DE 1999-19940765 19990827
DE 1999-19940768 19990827
DE 1999-19940831 19990827
DE 1999-19940832 19990827
DE 1999-19941385 19990831
DE 1999-19941396 19990831
DE 1999-19942087 19990903
US 1999-141031P 19990625 (60)
US 1999-143694P 19990714 (60)
US 1999-151778P 19990831 (60)

DT Utility

FS APPLICATION

LN.CNT 6552

INCL INCLM: 435/106.000
INCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
536/023.200

NCL NCLM: 435/106.000
NCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
536/023.200

IC [7]

ICM C12Q001-68
ICS C07H021-04; C12P013-04; C12N009-10; C12N001-21; C12N015-74
IPCI C12Q001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*]; C12N0009-10 [ICS,7];
C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7]
IPCR C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
C07K0014-34 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];

C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
C12P0001-04 [I,C*]; C12P0001-04 [I,A]; C12P0013-00 [I,C*];
C12P0013-04 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 15 OF 27 USPATFULL on STN
AN 2005:158196 USPATFULL
TI Nucleic acid and amino acid sequences relating to streptococcus
pneumoniae for diagnostics and therapeutics
IN Doucette-Stamm, Lynn A., Framingham, MA, UNITED STATES
Bush, David, Somerville, MA, UNITED STATES
PI US 20050136404 A1 20050623
AI US 2003-617320 A1 20030710 (10)
RLI Division of Ser. No. US 1998-107433, filed on 30 Jun 1998, PENDING
PRAI US 1997-51553P 19970702 (60)
US 1998-85131P 19980512 (60)
DT Utility
FS APPLICATION
LN.CNT 12957
INCL INCLM: 435/006.000
INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
NCL NCLM: 435/006.000
NCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
IC [7]
ICM C12Q001-68
ICS C07H021-04; C12N001-21; C07K014-315
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
C12N0001-21 [ICS,7]; C07K0014-315 [ICS,7]; C07K0014-195
[ICS,7,C*]
IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
C07K0014-195 [I,C*]; C07K0014-315 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 16-20

L5 ANSWER 16 OF 27 USPATFULL on STN
AN 2005:131152 USPATFULL
TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface
protein homologues and uses therefore
IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
Alterman, Eric, Apex, NC, UNITED STATES
Buck, B. Logan, Banner Elk, NC, UNITED STATES
Russell, W. Michael, Newburg, IN, UNITED STATES
PI US 20050112612 A1 20050526
US 7348420 B2 20080325
AI US 2004-831070 A1 20040423 (10)
PRAI US 2003-465621P 20030425 (60)
DT Utility
FS APPLICATION
LN.CNT 6100
INCL INCLM: 435/006.000
INCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 530/350.000;
536/023.200
NCL NCLM: 536/023.100; 435/006.000
NCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 530/350.000;
536/023.200
IC [7]
ICM C12Q001-68
ICS C07H021-04; C12P021-06; C12N009-00; C12N001-21; C07K014-335
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
C12P0021-06 [ICS,7]; C12N0009-00 [ICS,7]; C12N0001-21 [ICS,7];

C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
 IPCI-2 C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12N0001-20 [I,A];
 C12N0015-00 [I,A]; C12P0001-20 [I,A]
 IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
 C07K0014-335 [I,A]; C12N0001-20 [I,C]; C12N0001-20 [I,A];
 C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0009-00 [I,C*];
 C12N0009-00 [I,A]; C12N0015-00 [I,C]; C12N0015-00 [I,A];
 C12P0021-06 [I,C*]; C12P0021-06 [I,A]; C12Q0001-68 [I,C*];
 C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 27 USPATFULL on STN
 AN 2004:95339 USPATFULL
 TI Nutritional formulations containing synbiotic substances
 IN Kaup, Susan M., Collingswood, NJ, UNITED STATES
 Wilson, Jeffrey L., Doylestown, PA, UNITED STATES
 Kostek, Beverley M., Glen Mills, PA, UNITED STATES
 Frantz, David C., Pottstown, PA, UNITED STATES
 PA Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)
 PI US 20040072794 A1 20040415
 AI US 2003-681658 A1 20031008 (10)
 PRAI US 2002-418109P 20021011 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 542
 INCL INCLM: 514/054.000
 INCLS: 424/093.450
 NCL NCLM: 514/054.000
 NCLS: 424/093.450
 IC [7]
 ICM A61K045-00
 ICS A61K031-715
 IPCI A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]
 IPCR A23L0001-052 [I,C*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C*];
 A23L0001-29 [I,A]; A23L0001-30 [I,C*]; A23L0001-30 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 18 OF 27 USPATFULL on STN
 AN 2004:12970 USPATFULL
 TI Polynucleotides, materials incorporating them, and methods for using
 them
 IN Glenn, Matthew, Whenuapai, NEW ZEALAND
 Havukkala, Ilkka J., Remuera, NEW ZEALAND
 Lubbers, Mark, Palmerston North, NEW ZEALAND
 Dekker, James, Palmerston North, NEW ZEALAND
 PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND
 (non-U.S. corporation)
 PI US 20040009490 A1 20040115
 US 7125698 B2 20061024
 AI US 2002-264213 A1 20021003 (10)
 RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,
 PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug
 2000, GRANTED, Pat. No. US 6544772
 PRAI US 1999-147853P 19990809 (60)
 US 1999-147852P 19990809 (60)
 US 1999-152032P 19990901 (60)
 US 1999-152031P 19990901 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5375
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200

NCL NCLM: 435/193.000; 435/006.000
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;
 435/252.300; 435/320.100; 536/023.200

IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
 IPCI-2 C12N0009-10 [I,A]
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C*];
 A23C0019-032 [I,A]; A61K0038-00 [N,C*]; A61K0038-00 [N,A];
 C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 19 OF 27 USPATFULL on STN
 AN 2004:250212 USPATFULL
 TI Nucleic acid and amino acid sequences relating to Streptococcus
 pneumoniae for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn A., Framingham, MA, United States
 Bush, David, Somerville, MA, United States
 PA Genome Therapeutics Corporation, Waltham, MA, United States (U.S.
 corporation)
 PI US 6800744 B1 20041005
 AI US 1998-107433 19980630 (9)
 PRAI US 1998-85131P 19980512 (60)
 US 1997-51553P 19970702 (60)
 DT Utility
 FS GRANTED
 LN.CNT 11545
 INCL INCLM: 536/023.100
 INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;
 536/024.100; 536/023.400; 536/024.320

NCL NCLM: 536/023.100
 NCLS: 435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;
 536/024.100; 536/024.320

IC [7]
 ICM C12Q001-68
 ICS C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;
 C07H021-04
 IPCI C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];
 C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-315 [I,A]

EXF 536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;
 435/6

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 20 OF 27 USPATFULL on STN
 AN 2003:71519 USPATFULL
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
 Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
 Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF

PI US 20030049804 A1 20030313

AI US 2000-746660 A1 20001222 (9)
 RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
 PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
 2000, PENDING
 PRAI DE 1999-19931420 19990708
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 15004
 INCL INCLM: 435/115.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200
 NCL NCLM: 435/115.000
 NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200
 IC [7]
 ICM C12P013-08
 ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21
 IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
 C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
 C12N0001-21 [ICS,7]
 IPCR C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
 C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
 C12N0009-90 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 17

L5 ANSWER 17 OF 27 USPATFULL on STN
 AN 2004:95339 USPATFULL
 TI Nutritional formulations containing synbiotic substances
 IN Kaup, Susan M., Collingswood, NJ, UNITED STATES
 Wilson, Jeffrey L., Doylestown, PA, UNITED STATES
 Kostek, Beverley M., Glen Mills, PA, UNITED STATES
 Frantz, David C., Pottstown, PA, UNITED STATES
 PA Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)
 PI US 20040072794 A1 20040415
 AI US 2003-681658 A1 20031008 (10)
 PRAI US 2002-418109P 20021011 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 542
 INCL INCLM: 514/054.000
 INCLS: 424/093.450
 NCL NCLM: 514/054.000
 NCLS: 424/093.450
 IC [7]
 ICM A61K045-00
 ICS A61K031-715
 IPCI A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]
 IPCR A23L0001-052 [I,C*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C*];
 A23L0001-29 [I,A]; A23L0001-30 [I,C*]; A23L0001-30 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 17 ab

L5 ANSWER 17 OF 27 USPATFULL on STN
 AB Nutritional compositions are provided which comprise oligofructose,

sialyllactose and probiotic bacteria, which are useful in the eradication of pathogenic microorganisms in the gastrointestinal tracts of patients.

=> d 15 17 kwic

L5 ANSWER 17 OF 27 USPATFULL on STN

- SUMM [0004] Prebiotics are nondigestible food ingredients that that beneficially affect the host by selectively stimulating the growth and/or activity of one or a limited number. . . .
- SUMM [0011] Sialyllactose is known to have anti-adhesive properties for specific pathogenic bacteria. For example, sialyllactose acts to inhibit cholera toxin invitro (Idota et al., "Inhibition of Cholera Toxin by Human Milk Fractions and Sialyllactose," Biosci. Biotech. Biochem. 59:417-419) and Helicobacter pylori (Simon et al., "Inhibition of Helicobacter pylori Binding to Gastrointestinal Epithelial Cells by Sialic Acid-Containing Oligosaccharides," Infection and Immunity, 750-757, (1997)).
- SUMM [0015] Probiotics are live microbial food ingredients that have a beneficial effect on human health. (Salminen et al., "Functional food science and gastrointestinal physiology and function." Brit. J. Nutr. 80(suppl. 1):S147-S171 (1998)).
- SUMM . . . carbohydrate to lactic acid. The specific strains most often studied include members of the genera Lactobacillus and Bifidobacterium. (Sanders, "Probiotics." Food Technol. 53:67-77 (1999)).
- SUMM [0017] Some lactic acid bacteria specifically produce lactic acid as a major product of their metabolism. Some produce predominantly the levorotary "L"-form of lactic acid [L(+)-lactic acid], others produce predominantly the dextrorotary "D"-form. . . .
- SUMM [0019] A milk product containing LGG significantly shortened the duration of diarrhea in young children. (Kaila et al., "Enhancement of the circulating antibody secreting. . . .
- SUMM [0021] U.S. Pat. No. 5,908,646 discloses a method for inhibiting the growth or activity of Clostridium species in a human food product by adding an effective amount of the beneficial microorganism, L. rhamnosus [L. casei subspecies rhamnosus], which produces predominantly L(+)-lactic acid.
- SUMM . . . viable cells of three specific microorganisms beneficial to the human intestinal microorganisms for preventing diarrhea. Specifically, the three microorganisms are Lactobacillus reuteri, Lactobacillus acidophilus and Bifidobacterium infantis. The diarrhea can be caused by antibiotic treatment or by infection with a virus, a. . . .
- SUMM . . . "Bifidobacterium bifidum." (Fukushima et al., "Effect of a probiotic formula on intestinal immunoglobulin A production in healthy children." Int. J. Food Microb. 42-39-44 (1998)).

=> d 15 18

L5 ANSWER 18 OF 27 USPATFULL on STN

AN 2004:12970 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using them

IN Glenn, Matthew, Whenuapai, NEW ZEALAND
Havukkala, Ilkka J., Remuera, NEW ZEALAND
Lubbers, Mark, Palmerston North, NEW ZEALAND
Dekker, James, Palmerston North, NEW ZEALAND

PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND (non-U.S. corporation)

PI US 20040009490 A1 20040115
US 7125698 B2 20061024

AI US 2002-264213 A1 20021003 (10)
 RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,
 PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug
 2000, GRANTED, Pat. No. US 6544772
 PRAI US 1999-147853P 19990809 (60)
 US 1999-147852P 19990809 (60)
 US 1999-152032P 19990901 (60)
 US 1999-152031P 19990901 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 5375
 INCL INCLM: 435/006.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200
 NCL NCLM: 435/193.000; 435/006.000
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;
 435/252.300; 435/320.100; 536/023.200
 IC [7]
 ICM C12Q001-68
 ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
 IPCI-2 C12N0009-10 [I,A]
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C*];
 A23C0019-032 [I,A]; A61K0038-00 [N,C*]; A61K0038-00 [N,A];
 C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 19

L5 ANSWER 19 OF 27 USPATFULL on STN
 AN 2004:250212 USPATFULL
 TI Nucleic acid and amino acid sequences relating to Streptococcus
 pneumoniae for diagnostics and therapeutics
 IN Doucette-Stamm, Lynn A., Framingham, MA, United States
 Bush, David, Somerville, MA, United States
 PA Genome Therapeutics Corporation, Waltham, MA, United States (U.S.
 corporation)
 PI US 6800744 B1 20041005
 AI US 1998-107433 19980630 (9)
 PRAI US 1998-85131P 19980512 (60)
 US 1997-51553P 19970702 (60)
 DT Utility
 FS GRANTED
 LN.CNT 11545
 INCL INCLM: 536/023.100
 INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;
 536/024.100; 536/023.400; 536/024.320
 NCL NCLM: 536/023.100
 NCLS: 435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;
 536/024.100; 536/024.320
 IC [7]
 ICM C12Q001-68
 ICS C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;
 C07H021-04
 IPCI C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];
 C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
 C07K0014-195 [I,C*]; C07K0014-315 [I,A]

EXF 536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;
435/6

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 20-28

L5 ANSWER 20 OF 27 USPATFULL on STN

AN 2003:71519 USPATFULL

TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF

Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF

Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF

Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF

Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF

Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF

PI US 20030049804 A1 20030313

AI US 2000-746660 A1 20001222 (9)

RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
2000, PENDING

PRAI DE 1999-19931420 19990708

US 1999-141031P 19990625 (60)

US 1999-142101P 19990702 (60)

US 1999-148613P 19990812 (60)

US 2000-187970P 20000309 (60)

DT Utility

FS APPLICATION

LN.CNT 15004

INCL INCLM: 435/115.000

INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200

NCL NCLM: 435/115.000

NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200

IC [7]

ICM C12P013-08

ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21

IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
C12N0001-21 [ICS,7]

IPCR C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
C12N0009-90 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 21 OF 27 USPATFULL on STN

AN 2003:95966 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using
them

IN Glenn, Matthew, Auckland, NEW ZEALAND

Havukkala, Ilkka J., Auckland, NEW ZEALAND

Bloksberg, Leonard N., Auckland, NEW ZEALAND

Lubbers, Mark W., Palmerston North, NEW ZEALAND

Dekker, James, Palmerston North, NEW ZEALAND

Christensson, Anna C., Lund, SWEDEN

Holland, Ross, Palmerson North, NEW ZEALAND

O'Toole, Paul W., Palmerston North, NEW ZEALAND

Reid, Julian R., Palmerston North, NEW ZEALAND

Coolbear, Timothy, Palmerston North, NEW ZEALAND

PA Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.)

corporation)
 Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.
 corporation)
 PI US 6544772 B1 20030408
 AI US 2000-634238 20000808 (9)
 DT Utility
 FS GRANTED
 LN.CNT 2015
 INCL INCLM: 435/252.300
 INCLS: 435/320.100; 536/023.700
 NCL NCLM: 435/252.300
 NCLS: 435/320.100; 536/023.700
 IC [7]
 ICM C12N001-21
 ICS C12N015-63; C12N015-31
 IPCI C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]
 IPCR A23C0019-00 [I,C*]; A23C0019-032 [I,A]; C07K0014-195 [I,C*];
 C07K0014-335 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
 C12N0015-31 [I,C*]; C12N0015-31 [I,A]
 EXF 435/252.3; 435/320.1; 536/23.7
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN
 AN 1999-00562 BIOTECHDS
 TI Use of lactic and propionic acid bacteria;
 to bind mycotoxin to prevent their absorption or to purify
 contaminated food or feedstuff
 AU El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J
 PA Roy.Melbourne-Inst.Technol.
 LO Melbourne, Victoria, Australia.
 PI WO 9834503 13 Aug 1998
 AI WO 1998-AU63 6 Feb 1998
 PRAI AU 1997-5005 7 Feb 1997
 DT Patent
 LA English
 OS WPI: 1998-557001 [49]

L5 ANSWER 23 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): CP000705 GenBank (R)
 GenBank ACC. NO. (GBN): CP000705 AAOV01000000 AAOV01000001-AAOV01000097
 GenBank VERSION (VER): CP000705.1 GI:148530277
 SEQUENCE LENGTH (SQL): 1999618
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 17 Oct 2007
 DEFINITION (DEF): Lactobacillus reuteri F275,
 complete genome.
 SOURCE: Lactobacillus reuteri F275
 ORGANISM (ORGN): Lactobacillus reuteri F275
 Bacteria; Firmicutes; Lactobacillales;
 Lactobacillaceae; Lactobacillus
 PROJECT (PJID): GenomeProject:15766
 COMMENT:
 URL -- <http://www.jgi.doe.gov>
 JGI Project ID: 4000135
 Source DNA available from Gerald Tannock
 (gerald.tannock@stonebow.otago.ac.nz)
 Bacteria available from DSMZ: DSM 20016
 Contacts: Gerald Tannock (gerald.tannock@stonebow.otago.ac.nz)
 Paul Richardson (microbes@cuba.jgi-psf.org)
 Quality assurance done by JGI-Stanford

Annotation done by JGI-ORNL and JGI-PGF

Finishing done by JGI-PGF

Finished microbial genomes have been curated to close all gaps with greater than 98% coverage of at least two independent clones. Each base pair has a minimum q (quality) value of 30 and the total error rate is less than one per 50000.

The JGI and collaborators endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to follow them. It is our intention to publish the work of this project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>).

REFERENCE: 1 (bases 1 to 1999618)
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
TITLE (TI): Complete sequence of chromosome of
Lactobacillus reuteri DSM 20016
JOURNAL (SO): Unpublished
REFERENCE: 2 (bases 1 to 1999618)
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (17-MAY-2007) US DOE Joint Genome Institute,
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,
USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1999618	/organism="Lactobacillus reuteri F275" /mol-type="genomic DNA" /strain="DSM 20016" /db-xref="taxon:299033" /note="F275 = DSM 20016 = JCM 1112"

L5 ANSWER 24 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM270397 GenBank (R)
GenBank ACC. NO. (GBN): AM270397
GenBank VERSION (VER): AM270397.1 GI:134084136
CAS REGISTRY NO. (RN): 928607-03-8
SEQUENCE LENGTH (SQL): 163680
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Plants, fungi, algae
DATE (DATE): 24 Mar 2007
DEFINITION (DEF): Aspergillus niger contig An18c0040, complete genome.
SOURCE: Aspergillus niger
ORGANISM (ORGN): Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic
Trichocomaceae; Aspergillus
REFERENCE: 1 (bases 150631 to 153085)

AUTHOR (AU): Habison,A.; Kubicek,C.P.; Rohr,M.
 TITLE (TI): Partial purification and regulatory properties of
 phosphofructokinase from *Aspergillus niger*
 JOURNAL (SO): Biochem. J., 209 (3), 669-676 (1983)
 OTHER SOURCE (OS): CA 99:171737
 REFERENCE: 2 (bases 71863 to 73356)
 AUTHOR (AU): Manney,T.R.
 TITLE (TI): Expression of the BAR1 gene in *Saccharomyces*
cerevisiae: induction by the alpha mating pheromone of
 an activity associated with a secreted protein
 JOURNAL (SO): J. Bacteriol., 155 (1), 291-301 (1983)
 OTHER SOURCE (OS): CA 99:102121
 REFERENCE: 3 (bases 71863 to 73356)
 AUTHOR (AU): Jones,E.W.
 TITLE (TI): The synthesis and function of proteases in
Saccharomyces: genetic approaches
 JOURNAL (SO): Annu. Rev. Genet., 18, 233-270 (1984)
 OTHER SOURCE (OS): CA 102:92538
 REFERENCE: 4 (bases 144032 to 145578)
 AUTHOR (AU): Brandsch,R.; Bichler,V.
 TITLE (TI): In vivo and in vitro expression of the
 6-hydroxy-D-nicotine oxidase gene of *Arthrobacter*
oxidans, cloned into *Escherichia coli*, as an
 enzymatically active, covalently flavinylated
 polypeptide
 JOURNAL (SO): FEBS Lett., 192 (2), 204-208 (1985)
 OTHER SOURCE (OS): CA 104:29597
 REFERENCE: 5 (bases 150631 to 153085)
 AUTHOR (AU): Schreferl,G.; Kubicek,C.P.; Rohr,M.
 TITLE (TI): Inhibition of citric acid accumulation by manganese
 ions in *Aspergillus niger* mutants with reduced citrate
 control of phosphofructokinase
 JOURNAL (SO): J. Bacteriol., 165 (3), 1019-1022 (1986)
 OTHER SOURCE (OS): CA 104:165023
 REFERENCE: 6 (bases 156827 to 158638)
 AUTHOR (AU): Whittington,H.A.; Grant,S.; Roberts,C.F.; Lamb,H.;
 Hawkins,A.R.
 TITLE (TI): Identification and isolation of a putative permease
 gene in the quinic acid utilization (QUT) gene cluster
 of *Aspergillus nidulans*
 JOURNAL (SO): Curr. Genet., 12 (2), 135-139 (1987)
 OTHER SOURCE (OS): CA 107:91128
 REFERENCE: 7 (bases 54105 to 55762)
 AUTHOR (AU): Chisholm,V.T.; Lea,H.Z.; Rai,R.; Cooper,T.G.
 TITLE (TI): Regulation of allantate transport in wild-type and
 mutant strains of *Saccharomyces cerevisiae*
 JOURNAL (SO): J. Bacteriol., 169 (4), 1684-1690 (1987)
 OTHER SOURCE (OS): CA 106:172689
 REFERENCE: 8 (bases 71863 to 73356)
 AUTHOR (AU): MacKay,V.L.; Welch,S.K.; Insley,M.Y.; Manney,T.R.;
 Holly,J.; Saari,G.C.; Parker,M.L.
 TITLE (TI): The *Saccharomyces cerevisiae* BAR1 gene encodes an
 exported protein with homology to pepsin
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 85 (1), 55-59 (1988)
 OTHER SOURCE (OS): CA 108:125658
 REFERENCE: 9 (bases 54105 to 55762)
 AUTHOR (AU): Rai,R.; Genbauffe,F.S.; Cooper,T.G.
 TITLE (TI): Structure and transcription of the allantate permease
 gene (DAL5) from *Saccharomyces cerevisiae*
 JOURNAL (SO): J. Bacteriol., 170 (1), 266-271 (1988)
 OTHER SOURCE (OS): CA 109:17930
 REFERENCE: 10

AUTHOR (AU): Hawkins,A.R.; Lamb,H.K.; Smith,M.; Keyte,J.W.;
 Roberts,C.F.

TITLE (TI): Molecular organisation of the quinic acid utilization
 (QUT) gene cluster in *Aspergillus nidulans*

JOURNAL (SO): Mol. Gen. Genet., 214 (2), 224-231 (1988)

OTHER SOURCE (OS): CA 111:188522

REFERENCE: 11 (bases 68231 to 69040)

AUTHOR (AU): Honjo,M.; Nakayama,A.; Fukazawa,K.; Kawamura,K.;
 Ando,K.; Furutani,Y.

TITLE (TI): A novel *Bacillus subtilis* gene involved in negative
 control of sporulation and degradative-enzyme
 production

JOURNAL (SO): J. Bacteriol., 172 (4), 1783-1790 (1990)

OTHER SOURCE (OS): CA 113:146166

REFERENCE: 12 (bases 5212 to 7379)

AUTHOR (AU): Nikawa,J.; Hosaka,K.; Tsukagoshi,Y.; Yamashita,S.

TITLE (TI): Primary structure of the yeast choline transport gene
 and regulation of its expression

JOURNAL (SO): J. Biol. Chem., 265 (26), 15996-16003 (1990)

OTHER SOURCE (OS): CA 114:18549

REFERENCE: 13 (bases 159975 to 161849)

AUTHOR (AU): Fling,M.E.; Kopf,J.; Tamarkin,A.; Gorman,J.A.;
 Smith,H.A.; Koltin,Y.

TITLE (TI): Analysis of a *Candida albicans* gene that encodes a
 novel mechanism for resistance to benomyl and
 methotrexate

JOURNAL (SO): Mol. Gen. Genet., 227 (2), 318-329 (1991)

OTHER SOURCE (OS): CA 116:100405

REFERENCE: 14 (bases 28874 to 30837)

AUTHOR (AU): Masuda,N.; Kitamura,N.; Saito,K.

TITLE (TI): Primary structure of protein moiety of *Penicillium*
notatum phospholipase B deduced from the cDNA

JOURNAL (SO): Eur. J. Biochem., 202 (3), 783-787 (1991)

OTHER SOURCE (OS): CA 118:76020

REFERENCE: 15 (bases 100363 to 101496)

AUTHOR (AU): Sakoda,H.; Imanaka,T.

TITLE (TI): Cloning and sequencing of the gene coding for alcohol
 dehydrogenase of *Bacillus stearothermophilus* and
 rational shift of the optimum pH

JOURNAL (SO): J. Bacteriol., 174 (4), 1397-1402 (1992)

OTHER SOURCE (OS): CA 118:186708

REFERENCE: 16 (bases 20773 to 22555)

AUTHOR (AU): Kamoda,S.; Saburi,Y.

TITLE (TI): Structural and enzymatical comparison of
 lignostilbene-alpha,beta-dioxygenase isozymes, I, II,
 and III, from *Pseudomonas paucimobilis* TMY1009

JOURNAL (SO): Biosci. Biotechnol. Biochem., 57 (6), 931-934 (1993)

OTHER SOURCE (OS): CA 119:154577

REFERENCE: 17 (bases 80602 to 83154)

AUTHOR (AU): ElBerry,H.M.; Majumdar,M.L.; Cunningham,T.S.;
 Sumrada,R.A.; Cooper,T.G.

TITLE (TI): Regulation of the urea active transporter gene (DUR3)
 in *Saccharomyces cerevisiae*

JOURNAL (SO): J. Bacteriol., 175 (15), 4688-4698 (1993)

OTHER SOURCE (OS): CA 119:242524

REFERENCE: 18 (bases 23096 to 24052)

AUTHOR (AU): Roper,D.I.; Cooper,R.A.

TITLE (TI): Purification, nucleotide sequence and some properties
 of a bifunctional isomerase/decarboxylase from the
 homoprotocatechuate degradative pathway of *Escherichia*
coli C

JOURNAL (SO): Eur. J. Biochem., 217 (2), 575-580 (1993)

OTHER SOURCE (OS): CA 119:265270
REFERENCE: 19 (bases 5212 to 7379)
AUTHOR (AU): Li,Z.; Brendel,M.
TITLE (TI): Co-regulation with genes of phospholipid biosynthesis
of the CTR/HNM1-encoded choline/nitrogen mustard
permease in *Saccharomyces cerevisiae*
JOURNAL (SO): Mol. Gen. Genet., 241 (5-6), 680-684 (1993)
OTHER SOURCE (OS): CA 121:28475
REFERENCE: 20 (bases 159975 to 161849)
AUTHOR (AU): Ben-Yaacov,R.; Knoller,S.; Caldwell,G.A.; Becker,J.M.;
Koltin,Y.
TITLE (TI): *Candida albicans* gene encoding resistance to benomyl
and methotrexate is a multidrug resistance gene
JOURNAL (SO): Antimicrob. Agents Chemother., 38 (4), 648-652 (1994)
OTHER SOURCE (OS): CA 121:2236
REFERENCE: 21 (bases 150631 to 153085)
AUTHOR (AU): Legisa,M.; Bencina,M.
TITLE (TI): Evidence for the activation of 6-phosphofructo-1-kinase
by cAMP-dependent protein kinase in *Aspergillus niger*
JOURNAL (SO): FEMS Microbiol. Lett., 118 (3), 327-333 (1994)
OTHER SOURCE (OS): CA 121:102759
REFERENCE: 22 (bases 138020 to 140061)
AUTHOR (AU): Kim,Y.J.; Bjorklund,S.; Li,Y.; Sayre,M.H.;
Kornberg,R.D.
TITLE (TI): A multiprotein mediator of transcriptional activation
and its interaction with the C-terminal repeat domain
of RNA polymerase II
JOURNAL (SO): Cell, 77 (4), 599-608 (1994)
OTHER SOURCE (OS): CA 121:102149
REFERENCE: 23 (bases 38805 to 39836)
AUTHOR (AU): Downs,D.M.; Petersen,L.
TITLE (TI): *apbA*, a new genetic locus involved in thiamine
biosynthesis in *Salmonella typhimurium*
JOURNAL (SO): J. Bacteriol., 176 (16), 4858-4864 (1994)
OTHER SOURCE (OS): CA 121:197350
REFERENCE: 24 (bases 5212 to 7379)
AUTHOR (AU): Li,Z.; Brendel,M.
TITLE (TI): Sensitivity to nitrogen mustard in *Saccharomyces*
cerevisiae is independently determined by regulated
choline permease and DNA repair
JOURNAL (SO): Mutat. Res., 315 (2), 139-145 (1994)
OTHER SOURCE (OS): CA 121:198201
REFERENCE: 25 (bases 85096 to 90863)
AUTHOR (AU): Szczypka,M.S.; Wemmie,J.A.; Moye-Rowley,W.S.;
Thiele,D.J.
TITLE (TI): A yeast metal resistance protein similar to human
cystic fibrosis transmembrane conductance regulator
(CFTR) and multidrug resistance-associated protein
JOURNAL (SO): J. Biol. Chem., 269 (36), 22853-22857 (1994)
OTHER SOURCE (OS): CA 122:26140
REFERENCE: 26 (bases 91484 to 93088)
AUTHOR (AU): Knight,S.A.; Tamai,K.T.; Kosman,D.J.; Thiele,D.J.
TITLE (TI): Identification and analysis of a *Saccharomyces*
cerevisiae copper homeostasis gene encoding a
homeodomain protein
JOURNAL (SO): Mol. Cell. Biol., 14 (12), 7792-7804 (1994)
OTHER SOURCE (OS): CA 122:73697
REFERENCE: 27 (bases 85096 to 90863)
AUTHOR (AU): Wemmie,J.A.; Szczypka,M.S.; Thiele,D.J.;
Moye-Rowley,W.S.
TITLE (TI): Cadmium tolerance mediated by the yeast AP-1 protein
requires the presence of an ATP-binding cassette

transporter-encoding gene, YCF1

JOURNAL (SO): J. Biol. Chem., 269 (51), 32592-32597 (1994)

OTHER SOURCE (OS): CA 121:294343

REFERENCE: 28 (bases 20773 to 22555)

AUTHOR (AU): Kamoda,S.; Saburi,Y.

TITLE (TI): Cloning of a lignostilbene-alpha,beta-dioxygenase isozyme gene from *Pseudomonas paucimobilis* TMY1009

JOURNAL (SO): Biosci. Biotechnol. Biochem., 59 (10), 1866-1868 (1995)

OTHER SOURCE (OS): CA 124:47043

REFERENCE: 29 (bases 85096 to 90863)

AUTHOR (AU): Li,Z.S.; Szczypka,M.; Lu,Y.P.; Thiele,D.J.; Rea,P.A.

TITLE (TI): The yeast cadmium factor protein (YCF1) is a vacuolar glutathione S-conjugate pump

JOURNAL (SO): J. Biol. Chem., 271 (11), 6509-6517 (1996)

OTHER SOURCE (OS): CA 124:226108

REFERENCE: 30 (bases 33419 to 35477)

AUTHOR (AU): Silva,J.C.; Minto,R.E.; Barry,C.E. III; Holland,K.A.; Townsend,C.A.

TITLE (TI): Isolation and characterization of the versicolorin B synthase gene from *Aspergillus parasiticus*. Expansion of the aflatoxin b1 biosynthetic gene cluster

JOURNAL (SO): J. Biol. Chem., 271 (23), 13600-13608 (1996)

OTHER SOURCE (OS): CA 125:50401

REFERENCE: 31 (bases 15614 to 17392)

AUTHOR (AU): Covert,S.F.; Enkerli,J.; Miao,V.P.; VanEtten,H.D.

TITLE (TI): A gene for maackiain detoxification from a dispensable chromosome of *Nectria haematococca*

JOURNAL (SO): Mol. Gen. Genet., 251 (4), 397-406 (1996)

OTHER SOURCE (OS): CA 125:106677

REFERENCE: 32 (bases 131646 to 132375)

AUTHOR (AU): Mitsuhashi,S.; Miyachi,S.

TITLE (TI): Amino acid sequence homology between N- and C-terminal halves of a carbonic anhydrase in *Porphyridium purpureum*, as deduced from the cloned cDNA

JOURNAL (SO): J. Biol. Chem., 271 (45), 28703-28709 (1996)

OTHER SOURCE (OS): CA 125:321312

REFERENCE: 33 (bases 85096 to 90863)

AUTHOR (AU): Li,Z.S.; Lu,Y.P.; Zhen,R.G.; Szczypka,M.; Thiele,D.J.; Rea,P.A.

TITLE (TI): A new pathway for vacuolar cadmium sequestration in *Saccharomyces cerevisiae*: YCF1-catalyzed transport of bis(glutathionato)cadmium

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 94 (1), 42-47 (1997)

OTHER SOURCE (OS): CA 126:127966

REFERENCE: 34 (bases 1241 to 3043)

AUTHOR (AU): Saito,Y.; Ishii,Y.; Hayashi,H.; Imao,Y.; Akashi,T.; Yoshikawa,K.; Noguchi,Y.; Soeda,S.; Yoshida,M.; Niwa,M.; Hosoda,J.; Shimomura,K.

TITLE (TI): Cloning of genes coding for L-sorbose and L-sorbose dehydrogenases from *Gluconobacter oxydans* and microbial production of 2-keto-L-gulonate, a precursor of L-ascorbic acid, in a recombinant *G. oxydans* strain

JOURNAL (SO): Appl. Environ. Microbiol., 63 (2), 454-460 (1997)

OTHER SOURCE (OS): CA 126:167180

REFERENCE: 35 (bases 150631 to 153085)

AUTHOR (AU): Ruijter,G.J.; Panneman,H.; Visser,J.

TITLE (TI): Overexpression of phosphofructokinase and pyruvate kinase in citric acid-producing *Aspergillus niger*

JOURNAL (SO): Biochim. Biophys. Acta, 1334 (2-3), 317-326 (1997)

OTHER SOURCE (OS): CA 126:222695

REFERENCE: 36 (bases 49850 to 51919)

AUTHOR (AU): Prieto,R.; Woloshuk,C.P.

TITLE (TI): ord1, an oxidoreductase gene responsible for conversion of O-methylsterigmatocystin to aflatoxin in *Aspergillus flavus*
 JOURNAL (SO): Appl. Environ. Microbiol., 63 (5), 1661-1666 (1997)
 OTHER SOURCE (OS): CA 127:13942
 REFERENCE: 37 (bases 17766 to 20491)
 AUTHOR (AU): Todd,R.B.; Murphy,R.L.; Martin,H.M.; Sharp,J.A.; Davis,M.A.; Katz,M.E.; Hynes,M.J.
 TITLE (TI): The acetate regulatory gene facB of *Aspergillus nidulans* encodes a Zn(II)2Cys6 transcriptional activator
 JOURNAL (SO): Mol. Gen. Genet., 254 (5), 495-504 (1997)
 OTHER SOURCE (OS): CA 127:105007
 REFERENCE: 38 (bases 71863 to 73356)
 AUTHOR (AU): Ballensiefen,W.; Schmitt,H.D.
 TITLE (TI): Periplasmic Bar1 protease of *Saccharomyces cerevisiae* is active before reaching its extracellular destination
 JOURNAL (SO): Eur. J. Biochem., 247 (1), 142-147 (1997)
 OTHER SOURCE (OS): CA 127:187926
 REFERENCE: 39 (bases 52148 to 53720)
 AUTHOR (AU): Kuroyanagi,N.; Onogi,H.; Wakabayashi,T.; Hagiwara,M.
 TITLE (TI): Novel SR-protein-specific kinase, SRPK2, disassembles nuclear speckles
 JOURNAL (SO): Biochem. Biophys. Res. Commun., 242 (2), 357-364 (1998)
 OTHER SOURCE (OS): CA 128:241040
 REFERENCE: 40 (bases 113565 to 114733)
 AUTHOR (AU): MacDiarmid,C.W.; Gardner,R.C.
 TITLE (TI): Overexpression of the *Saccharomyces cerevisiae* magnesium transport system confers resistance to aluminum ion
 JOURNAL (SO): J. Biol. Chem., 273 (3), 1727-1732 (1998)
 OTHER SOURCE (OS): CA 128:177021
 REFERENCE: 41 (bases 135940 to 137166)
 AUTHOR (AU): Wang,H.Y.; Lin,W.; Dyck,J.A.; Yeakley,J.M.; Songyang,Z.; Cantley,L.C.; Fu,X.D.
 TITLE (TI): SRPK2: a differentially expressed SR protein-specific kinase involved in mediating the interaction and localization of pre-mRNA splicing factors in mammalian cells
 JOURNAL (SO): J. Cell Biol., 140 (4), 737-750 (1998)
 OTHER SOURCE (OS): CA 128:306636
 REFERENCE: 42 (bases 38805 to 39836)
 AUTHOR (AU): Frodyma,M.E.; Downs,D.
 TITLE (TI): ApbA, the ketopantoate reductase enzyme of *Salmonella typhimurium* is required for the synthesis of thiamine via the alternative pyrimidine biosynthetic pathway
 JOURNAL (SO): J. Biol. Chem., 273 (10), 5572-5576 (1998)
 OTHER SOURCE (OS): CA 128:305459
 REFERENCE: 43 (bases 106231 to 106803)
 AUTHOR (AU): Woloshuk,C.P.; Prieto,R.
 TITLE (TI): Genetic organization and function of the aflatoxin B1 biosynthetic genes
 JOURNAL (SO): FEMS Microbiol. Lett., 160 (2), 169-176 (1998)
 OTHER SOURCE (OS): CA 128:290649
 REFERENCE: 44 (bases 93571 to 94963)
 AUTHOR (AU): Philp,N.J.; Yoon,H.; Grollman,E.F.
 TITLE (TI): Monocarboxylate transporter MCT1 is located in the apical membrane and MCT3 in the basal membrane of rat RPE
 JOURNAL (SO): Am. J. Physiol., 274 (6 PT 2), R1824-R1828 (1998)
 OTHER SOURCE (OS): CA 129:159493
 REFERENCE: 45 (bases 93571 to 94963)

AUTHOR (AU): Wilson,M.C.; Jackson,V.N.; Heddle,C.; Price,N.T.;
Pilegaard,H.; Juel,C.; Bonen,A.; Montgomery,I.;
Hutter,O.F.; Halestrap,A.P.

TITLE (TI): Lactic acid efflux from white skeletal muscle is
catalyzed by the monocarboxylate transporter isoform
MCT3

JOURNAL (SO): J. Biol. Chem., 273 (26), 15920-15926 (1998)

OTHER SOURCE (OS): CA 129:159801

REFERENCE: 46 (bases 153410 to 154508)

AUTHOR (AU): Dekkers,L.C.; van der Bij,A.J.; Mulders,I.H.;
Phoelich,C.C.; Wentwoord,R.A.; Glandorf,D.C.;
Wijffelman,C.A.; Lugtenberg,B.J.

TITLE (TI): Role of the O-antigen of lipopolysaccharide, and
possible roles of growth rate and of NADH:ubiquinone
oxidoreductase (nuo) in competitive tomato root-tip
colonization by *Pseudomonas fluorescens* WCS365

JOURNAL (SO): Mol. Plant Microbe Interact., 11 (8), 763-771 (1998)

OTHER SOURCE (OS): CA 129:200426

REFERENCE: 47 (bases 146433 to 148685)

AUTHOR (AU): Saito,K.; Yamazaki,H.; Ohnishi,Y.; Fujimoto,S.;
Takahashi,E.; Horinouchi,S.

TITLE (TI): Production of trehalose synthase from a basidiomycete,
Grifola frondosa, in *Escherichia coli*

JOURNAL (SO): Appl. Microbiol. Biotechnol., 50 (2), 193-198 (1998)

OTHER SOURCE (OS): CA 130:956

REFERENCE: 48 (bases 122486 to 123895)

AUTHOR (AU): Kimura,M.; Matsumoto,G.; Shingu,Y.; Yoneyama,K.;
Yamaguchi,I.

TITLE (TI): The mystery of the trichothecene 3-O-acetyltransferase
gene. Analysis of the region around Tri101 and
characterization of its homologue from *Fusarium*
sporotrichioides

JOURNAL (SO): FEBS Lett., 435 (2-3), 163-168 (1998)

OTHER SOURCE (OS): CA 130:11163

REFERENCE: 49 (bases 146433 to 148685)

AUTHOR (AU): Saito,K.; Kase,T.; Takahashi,E.; Horinouchi,S.

TITLE (TI): Purification and characterization of a trehalose
synthase from the basidiomycete *grifola frondosa*

JOURNAL (SO): Appl. Environ. Microbiol., 64 (11), 4340-4345 (1998)

OTHER SOURCE (OS): CA 130:34870

REFERENCE: 50 (bases 14029 to 15172)

AUTHOR (AU): Feng,Y.; Khoo,H.E.; Poh,C.L.

TITLE (TI): Purification and characterization of gentisate
1,2-dioxygenases from *Pseudomonas alcaligenes* NCIB 9867
and *Pseudomonas putida* NCIB 9869

JOURNAL (SO): Appl. Environ. Microbiol., 65 (3), 946-950 (1999)

OTHER SOURCE (OS): CA 130:322223

REFERENCE: 51 (bases 59070 to 60560)

AUTHOR (AU): Bosch,R.; Moore,E.R.; Garcia-Valdes,E.; Pieper,D.H.

TITLE (TI): NahW, a novel, inducible salicylate hydroxylase
involved in mineralization of naphthalene by
Pseudomonas stutzeri AN10

JOURNAL (SO): J. Bacteriol., 181 (8), 2315-2322 (1999)

OTHER SOURCE (OS): CA 131:70144

REFERENCE: 52

AUTHOR (AU): DeZwaan,T.M.; Carroll,A.M.; Valent,B.; Sweigard,J.A.

TITLE (TI): *Magnaporthe grisea* pth11p is a novel plasma membrane
protein that mediates appressorium differentiation in
response to inductive substrate cues

JOURNAL (SO): Plant Cell, 11 (10), 2013-2030 (1999)

OTHER SOURCE (OS): CA 132:47358

REFERENCE: 53 (bases 122486 to 123895)

AUTHOR (AU): McCormick, S.P.; Alexander, N.J.; Trapp, S.E.; Hohn, T.M.
 TITLE (TI): Disruption of TRI101, the gene encoding trichothecene 3-O-acetyltransferase, from *Fusarium sporotrichioides*
 JOURNAL (SO): Appl. Environ. Microbiol., 65 (12), 5252-5256 (1999)
 OTHER SOURCE (OS): CA 132:118174
 REFERENCE: 54 (bases 111907 to 113460)
 AUTHOR (AU): Muraguchi, H.; Kamada, T.
 TITLE (TI): A mutation in the *eln2* gene encoding a cytochrome P450 of *Coprinus cinereus* affects mushroom morphogenesis
 JOURNAL (SO): Fungal Genet. Biol., 29 (1), 49-59 (2000)
 OTHER SOURCE (OS): CA 134:96073
 REFERENCE: 55 (bases 108826 to 111209)
 AUTHOR (AU): Yu, J.; Chang, P.K.; Bhatnagar, D.; Cleveland, T.E.
 TITLE (TI): Genes encoding cytochrome P450 and monooxygenase enzymes define one end of the aflatoxin pathway gene cluster in *Aspergillus parasiticus*
 JOURNAL (SO): Appl. Microbiol. Biotechnol., 53 (5), 583-590 (2000)
 OTHER SOURCE (OS): CA 133:291807
 REFERENCE: 56 (bases 122486 to 123895)
 AUTHOR (AU): Muhitch, M.J.; McCormick, S.P.; Alexander, N.J.; Hohn, T.M.
 TITLE (TI): Transgenic expression of the TRI101 or PDR5 gene increases resistance of tobacco to the phytotoxic effects of the trichothecene 4,15-diacetoxyscirpenol
 JOURNAL (SO): Plant Sci., 157 (2), 201-207 (2000)
 OTHER SOURCE (OS): CA 133:306551
 REFERENCE: 57 (bases 107279 to 108340)
 AUTHOR (AU): Cheng, Q.; Thomas, S.M.; Kostichka, K.; Valentine, J.R.; Nagarajan, V.
 TITLE (TI): Genetic analysis of a gene cluster for cyclohexanol oxidation in *Acinetobacter* sp. Strain SE19 by in vitro transposition
 JOURNAL (SO): J. Bacteriol., 182 (17), 4744-4751 (2000)
 OTHER SOURCE (OS): CA 134:37832
 REFERENCE: 58 (bases 100363 to 101496)
 AUTHOR (AU): Jornvall, H.; Hoog, J.O.; Persson, B.; Pares, X.
 TITLE (TI): Pharmacogenetics of the alcohol dehydrogenase system
 JOURNAL (SO): Pharmacology, 61 (3), 184-191 (2000)
 OTHER SOURCE (OS): CA 134:38655
 REFERENCE: 59
 AUTHOR (AU): Calabrese, D.; Bille, J.; Sanglard, D.
 TITLE (TI): A novel multidrug efflux transporter gene of the major facilitator superfamily from *Candida albicans* (FLU1) conferring resistance to fluconazole
 JOURNAL (SO): Microbiology (Reading, Engl.), 146 (PT 11), 2743-2754 (2000)
 OTHER SOURCE (OS): CA 135:1055
 REFERENCE: 60
 AUTHOR (AU): Deising, H.B.; Werner, S.; Wernitz, M.
 TITLE (TI): The role of fungal appressoria in plant infection
 JOURNAL (SO): Microbes Infect., 2 (13), 1631-1641 (2000)
 REFERENCE: 61 (bases 43783 to 45994)
 AUTHOR (AU): Smith, S.
 TITLE (TI): The world according to PARP
 JOURNAL (SO): Trends Biochem. Sci., 26 (3), 174-179 (2001)
 OTHER SOURCE (OS): CA 135:15779
 REFERENCE: 62 (bases 131646 to 132375)
 AUTHOR (AU): Cronk, J.D.; Endrizzi, J.A.; Cronk, M.R.; O'Neill, J.W.; Zhang, K.Y.
 TITLE (TI): Crystal structure of *E. coli* beta-carbonic anhydrase, an enzyme with an unusual pH-dependent activity
 JOURNAL (SO): Protein Sci., 10 (5), 911-922 (2001)
 REFERENCE: 63 (bases 43783 to 45994)

AUTHOR (AU): Ziegler,M.; Oei,S.L.
 TITLE (TI): A cellular survival switch: poly(ADP-ribosyl)ation stimulates DNA repair and silences transcription
 JOURNAL (SO): Bioessays, 23 (6), 543-548 (2001)
 REFERENCE: 64 (bases 43783 to 45994)
 AUTHOR (AU): Herceg,Z.; Wang,Z.Q.
 TITLE (TI): Functions of poly(ADP-ribose) polymerase (PARP) in DNA repair, genomic integrity and cell death
 JOURNAL (SO): Mutat. Res., 477 (1-2), 97-110 (2001)
 OTHER SOURCE (OS): CA 136:145570
 REFERENCE: 65 (bases 15614 to 17392)
 AUTHOR (AU): Mundodi,S.R.; Watson,B.S.; Lopez-Meyer,M.; Paiva,N.L.
 TITLE (TI): Functional expression and subcellular localization of the Nectria haematococca Mak1 phytoalexin detoxification enzyme in transgenic tobacco
 JOURNAL (SO): Plant Mol. Biol., 46 (4), 421-432 (2001)
 OTHER SOURCE (OS): CA 135:285870
 REFERENCE: 66 (bases 1 to 163680)
 AUTHOR (AU): Pel,H.J.; de Winde,J.H.; Archer,D.B.; Dyer,P.S.; Hofmann,G.; Schaap,P.J.; Turner,G.; de Vries,R.P.; Albang,R.; Albermann,K.; Andersen,M.R.; Bendtsen,J.D.; Benen,J.A.; van den Berg,M.; Breestraat,S.; Caddick,M.X.; Contreras,R.; Cornell,M.; Coutinho,P.M.; Danchin,E.G.; Debets,A.J.; Dekker,P.; van Dijck,P.W.; van Dijk,A.; Dijkhuizen,L.; Driessen,A.J.; d'Enfert,C.; Geysens,S.; Goosen,C.; Groot,G.S.; de Groot,P.W.; Guillemette,T.; Henrissat,B.; Herweijer,M.; van den Hombergh,J.P.; van den Hondel,C.A.; van der Heijden,R.T.; van der Kaaij,R.M.; Klis,F.M.; Kools,H.J.; Kubicek,C.P.; van Kuyk,P.A.; Lauber,J.; Lu,X.; van der Maarel,M.J.; Meulenberg,R.; Menke,H.; Mortimer,M.A.; Nielsen,J.; Oliver,S.G.; Olsthoorn,M.; Pal,K.; van Peij,N.N.; Ram,A.F.; Rinas,U.; Roubos,J.A.; Sagt,C.M.; Schmoll,M.; Sun,J.; Ussery,D.; Varga,J.; Vervecken,W.; van de Vondervoort,P.J.; Wedler,H.; Wosten,H.A.; Zeng,A.P.; van Ooyen,A.J.; Visser,J.; Stam,H.
 TITLE (TI): Genome sequencing and analysis of the versatile cell factory *Aspergillus niger* CBS 513.88
 JOURNAL (SO): Nat. Biotechnol., 25 (2), 221-231 (2007)
 OTHER SOURCE (OS): CA 146:310276
 REFERENCE: 67 (bases 1 to 163680)
 AUTHOR (AU): Pel,H.J.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O. Box 1, 2600 MA Delft, THE NETHERLANDS

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..163680	/organism="Aspergillus niger" /mol-type="genomic DNA" /db-xref="taxon:5061" /clone="An18c0040"
gene	<41..>545	/locus-tag="An18g00920"
mRNA	join(<41..325, 417..>545)	/locus-tag="An18g00920"
CDS	join(41..325,417..545)	/locus-tag="An18g00920" /codon-start=1 /product="hypothetical protein" /protein-id="CAK47170.1" /db-xref="GI:134084137"

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exon	41..325	/locus-tag="An18g00920"
		/number=1
intron	326..416	/locus-tag="An18g00920"
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exon	417..545	/locus-tag="An18g00920"
		/number=2
gene	874..954	/gene="tRNA-Arg (CCG)"
		/locus-tag="An18e00930"
tRNA	874..954	/gene="tRNA-Arg (CCG)"
		/locus-tag="An18e00930"
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mRNA	complement(join(<1241..	/locus-tag="An18g00940"
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	1867..2175,2229..2599,	
	2960..>3043))	
CDS	complement(join(1241..1	/locus-tag="An18g00940"
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	1867..2175,2229..2599,	
	2960..3043))	
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		/inference="profile:PFAM:PF05199"
		/note="unnamed protein product;
		Catalytic activity: L-sorbose +
		acceptor <=> 5-dehydro-D-fructose
		+ reduced acceptor. Cofactor: FAD.
		Title: strong similarity to FAD
		dependent L-sorbose dehydrogenase
		SDH - Gluconobacter oxydans"
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		/codon-start=1
		/protein-id="CAK47171.1"
		/db-xref="GI:134084138"
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intron	complement(1274..1324)	/locus-tag="An18g00940"

exon	complement(1325..1814)	/number=1 /locus-tag="An18g00940"
intron	complement(1815..1866)	/number=2 /locus-tag="An18g00940"
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intron	complement(2176..2228)	/number=3 /locus-tag="An18g00940"
exon	complement(2229..2599)	/number=3 /locus-tag="An18g00940"
intron	complement(2600..2959)	/number=4 /locus-tag="An18g00940"
exon	complement(2960..3043)	/number=4 /locus-tag="An18g00940"
gene	complement(<3788..>4775)	/number=5 /locus-tag="An18g00950"
mRNA	complement(join(<3788..4122,4201..4523,4678..>4775))	/locus-tag="An18g00950"
CDS	complement(join(3788..4122,4201..4523,4678..4775))	/locus-tag="An18g00950"
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		MK0549 - Methanopyrus kandle"
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		QPLSCTWYPEGSERAHEYASRMLSQAFFPRMCWLQ
		RPHAGVNAMGVHPDYRRRGVGRLL
		MQWGHHERIDPLGYESWIEGSPIGRWLYEESGYKR
		VISLNIDFAKKNPSEWNRLVHEC
		QPPAILLLWRPPRGEWNDKVPPGPWAVTETDHWK"
exon	complement(3788..4122)	/locus-tag="An18g00950"
intron	complement(4123..4200)	/number=1 /locus-tag="An18g00950"
exon	complement(4201..4523)	/number=1 /locus-tag="An18g00950"
intron	complement(4524..4677)	/number=2 /locus-tag="An18g00950"
exon	complement(4678..4775)	/number=2 /locus-tag="An18g00950"
gene	complement(<5212..>7379)	/number=3 /locus-tag="An18g00960"
mRNA	complement(join(<5212..5456,5493..5664,5746..6075,6140..6159,6225..6602,6674..6746,6800..6899,7249..>7379))	/locus-tag="An18g00960"
CDS	complement(join(5212..5456,5493..5664,5746..6075,6140..6159,6225..6602,6674..6746,6800..6899,7249..7379))	/locus-tag="An18g00960"

456,5493..5664,
5746..6075,6140..6159,
6225..6602,6674..6746,
6800..6899,7249..7379))

/inference="profile:COGS:COG0833"
/inference="similar to AA
sequence:PIR:S11175"
/note="unnamed protein product;
Function: Hnml of *S. cerevisiae* is
the unique coline permease in
yeast (Km of 0.5 micromolar).
Regulation: in *S. cerevisiae*,
expression of HNM1 gene is
regulated by the phospholipid
precursors inositol and choline
and this regulation involves the
trans-acting factors Ino2p, Ino4p
and Opilp. Remark: alternate name
for *S. cerevisiae* Hnml is YGL077c.
Similarity: Hnml of *S. cerevisiae*
belongs to the APC family, which
encompasses amino acid permeases
more related to the mammalian
cationic amino-acid transporter
family (Tea/ecoR). Title: strong
similarity to choline permease
Hnml -*Saccharomyces cerevisiae*
plasma membrane"
/citation=[12]
/citation=[19]
/citation=[24]
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GGPAGLVYGFGLGVWAGIISVFISMGELASMMPSA
GGQYHWVSILAPRSARKFLSHVTG
SVCIIAWTAAPTAAYLAASVLQSTIAMNIPSYD
PKGWHITLIMWAILLVCTVLNTWL
GMILPVIEVLILLVHVLGFFAVLVPLVYLGPKAD
PRSIFTVSFDYGGWGDLTATFIG
LKGTVAAFVGTGDGAVHMAEEVANSSRVVPRSMML
ALMINGATGFAILIAFLFTAGDLL
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LQACAGLAGISSGSRMLWSFSREQ
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exon	complement(5212..5456)	/locus-tag="An18g00960" /number=1
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intron	complement(5665..5745)	/locus-tag="An18g00960" /number=2
exon	complement(5746..6075)	/locus-tag="An18g00960" /number=3
intron	complement(6076..6139)	/locus-tag="An18g00960"

exon	complement(6140..6159)	/number=3 /locus-tag="An18g00960"
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intron	complement(6603..6673)	/number=5 /locus-tag="An18g00960"
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gene	complement(<7770..>8415	/number=8 /locus-tag="An18g00970"
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intron	complement(8283..8379)	/number=1 /locus-tag="An18g00970"
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		<p>Pth11-green fluorescent protein fusion localised to the cell membrane and vacuoles. Similarity: similarity of the predicted A. niger protein and M. grisea Pth11 is limited to the N-terminal half of the protein sequences. Title: weak similarity to integral membrane protein PTH11 - Magnaporthe grisea plasma membrane"</p> <p>/citation=[52]</p> <p>/codon-start=1</p> <p>/protein-id="CAK47175.1"</p> <p>/db-xref="GI:134084142"</p> <p>/translation="MTDHSAAVKVVTCTLLIVSF IAVVACLTNNQVLRKVVSSVALL LSTLIASIASGAAVSVAATHGLGQASPLTDAQVV VMQKALYSMEVLYVLTGLGLKLSV MVLFYSLSSSTGQSKSVLAATGLLLIWWVVMVIV VCLQCHPPEVWNIVGGTCLDLGI WIAFGVMNVLVEIMIIAVPSFIIIFRLKLSLKRRRL VVISCFGIRILDIAGSIVQLCYVR NFKIHADSPMPTNVWQWAICSQVLQTVAILSACV PYLREFLESFSPGMFKPTCLKHPT VQSAYNATKCSDSIELMRPESTKDT"</p>
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CDS	join(10500..10749, 10812..11041, 11105..11479)	/locus-tag="An18g01000" /note="unnamed protein product; Similarity: the nucleotide sequence of the ORF shows strong similarity to the ESTs an-2192 and an-2204 of A. niger. Title: strong similarity to EST an-2192 -Aspergillus niger" /codon-start=1 /protein-id="CAK47177.1" /db-xref="GI:134084144" /translation="MYSYEKVNRRDDSDQGLLAE DSERVAPQPRVSRFPSWTNALLLL GLLFSLSLNVGWVVFQKGHNVP IQDLDPDAAMAK QRSPYTGLAWDTHKPYSHHSEYTS ENATHADEMWESLSMDPMVIAPTWEWAQSKGLSD SWAFPWDSNRRIYFIKVFHQLHCL KLMRHSYHELWSGQESSIPAPHIEHCLDSL RQDL MCKADDTMPPSLQLLNGGGEGQQM QCKDFDKLVAWSKAPERNACYKRLTDYKPIVHSI ERYAFCPEDSEHYPTMSKYFEEHG HYADPFSE"
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intron	10750..10811	/locus-tag="An18g01000" /number=1
exon	10812..11041	/locus-tag="An18g01000" /number=2
intron	11042..11104	/locus-tag="An18g01000" /number=2
exon	11105..11479	/locus-tag="An18g01000" /number=3
gene	<11980..>13464	/locus-tag="An18g01010"
mRNA	join(<11980..12137, 12198..>13464)	/locus-tag="An18g01010"
CDS	join(11980..12137, 12198..13464)	/locus-tag="An18g01010" /inference="profile:COGS:COG0477" /note="unnamed protein product; Function: FLU1 of C. albicans facilitates resistance to fluconazole and cycloheximide in the fluconazole-hypersensitive S. cerevisiae strain YKKB-13 lacking the ABC (ATP-binding cassette) transporter gene PDR5. Function: FLU1 of C. albicans facilitates resistance to mycophenolic acid in C. albicans. Function: FLU1 of C. albicans is involved in the resistance to azol derivatives in C. albicans. Function: MDR1 of C.

albicans facilitates resistance to the anti-mitotic drug benomyl and to the dihydrofolate reductase inhibitor methotrexate. Similarity: N-terminus of the A. niger protein is app. 120 aa shorter than in FLU1 of C. albicans. Similarity: the predicted A. niger protein shows strong similarity to fluconazole resistance protein FLU1 of C. albicans, which is a permease belonging to the major facilitator superfamily. Title: strong similarity to fluconazole resistance protein FLU1 - Candida albicans"

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LYGRQWPLNIANLFFVAFLAGTAASTSIQMLIAF
RFLSGAATAASAIGPGIVSDLFPE
ESRGRAMSIMSLTGALGPVVGPIIGSYLGEKAGW
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FKAILRPLRLLIRSPMLILVTFYL
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GLCLGLILGAFLCSFLLDRYVRTA
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CDS	complement(join(14029..14318,14411..14845,14917..15172))	/locus-tag="An18g01020"

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/inference="similar to AA
sequence:UniProtKB:AF173167.3"
/note="unnamed protein product;
Complex: the estimated molecular
mass of the purified gentisate 1,
2-dioxygenase of P. alcaligenes
was 154 kDa, with a subunit mass
of 39 kDa. its structure is

deduced to be a tetramer. Remark:
 gentisate 1,2-dioxygenase of P.
 alcaligenes exhibits typical
 saturation kinetics and has an
 apparent Km of 92 microM for
 gentisate. this enzyme has broad
 substrate specificities towards
 alkyl and halogenated gentisate
 analogs. Similarity: the predicted
 A. niger protein shows strong
 similarity to gentisate
 1,2-dioxygenase of P. alcaligenes
 and conserved hypothetical
 proteins from other procaryotic
 species. Title: strong similarity
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 - Pseudomonas alcaligenes"
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 PNETAPAHRHTAFAMRYIIIEGNGGFTAVHGKRIK
 MQKGDVILTPTWNYHDHGKDGTP
 MIWLDGLDLPNFRHFPVHFVDHYDQPRYPADVD
 SATSPIVFPWDKMKAEKDKAPGTW
 AVRRYL RADGSEGSAERVDAGTSSLPRQET TSA
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intron	complement(14846..14916	/locus-tag="An18g01020"
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		/number=2
exon	complement(14917..15172	/locus-tag="An18g01020"
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	15723..16281,	
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	16584..16739,	
	16803..16942,	
	17034..>17392)	
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	16347..16503,	
	16584..16739,	
	16803..16942,	
	17034..17392)	
		/inference="profile:COGS:COG0654"

/inference="profile:PFAM:PF01360"
 /note="unnamed protein product;
 Function: Mak1 from N.
 haematococca specifically
 hydroxylates the phytoalexins
 medicarpin and
 maackiain, converting them to less
 fungitoxic derivatives.
 Localization: heterologous
 expression of the Mak1 cDNA
 construct in plants indicated that
 Mak1 protein accumulates in the
 plant cytoplasm, associated with
 endoplasmic reticulum membranes.
 Similarity: the predicted A. niger
 protein shows strong similarity to
 Mak1 from the fungal pathogen N.
 haematococca. Mak1 belongs to the
 flavin-containing mono-oxygenases.
 best matches are with putative
 salicylate hydroxylases of several
 procaryotic species. Title: strong
 similarity to maackiain
 detoxification protein 1 MAK1 -
 Nectria haematococca endoplasmatic
 reticulum"
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 NFVNNFKAPYYVIHRADFHSALCQ
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 ADLIVAADGIKSVARNVVLQGDEM
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 NIWIGDSRHVMTYTIGAGKAFNMV
 LSHPEMTDPGTWKPETALEDMKAEFQGWDPILSK
 IIGMVEKTVKWPLLTGTLLQNWTV
 GKLVI LGDAAHAMVPYMSQGAAMAVEDGIALSRS
 LSHMTSRDQLQKALSIFQEVKKR
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exon	16803..16942	/locus-tag="An18g01030"
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intron	16943..17033	/locus-tag="An18g01030"
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mRNA	join(<17766..17864, 17939..18039, 18108..18343, 18398..19163, 19373..19935, 20037..20252, 20325..>20491)	/locus-tag="An18g01040"
CDS	join(17766..17864, 17939..18039, 18108..18343, 18398..19163, 19373..19935, 20037..20252, 20325..20491)	

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 /note="unnamed protein product;
 Phenotype: facB recessive loss of
 function mutants in A. nidulans
 are deficient in acetate induction
 of acetyl-CoA synthase, isocitrate
 lyase, malate
 synthase, acetamidase, and
 NADP-isocitrate dehydrogenase.
 Similarity: the predicted A. niger
 protein shows similarity to
 acetate regulatory DNA binding
 protein FacB (facB) from A.
 nidulans, which belongs to the
 GAL4-type zinc cluster
 transcriptional activators. Title:
 similarity to acetate regulatory
 DNA binding protein facB -
 Aspergillus nidulans"
 /citation=[37]
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 LETSMATVKSDLGSGFASQINGSMP
 DAPRKENPLSNQSERFSDFAGTEDTIDAMGAVAF
 ADEEDCGFFGPSSNIAFLRHLSCA
 VAHSASAQKEITSPPLDRVAYDGGFVSATRPSSP
 SHDQRPESELEGEKFDKFALPPPEE
 SLALIHRYFADTGLLFPYIHPPTFFETYAELKDN
 SKRVRRTWLGLLNIIILAMAKLTAV
 SGT TSAETGISESAIYYHRALSLCKGEILRGTTL
 EVGRYSIYAPVRARVPVYL RATKI
 NTVQYLLVMGQYLGQTQKSVQAWTIHGLAVKAAL
 QLGLHSGASRAFTPLEQEVRKRT

		WFGCVVLDVRANLFLNKRKTIQQANIRVSTLYK QIANIIDRIYGQNLGCDSPLSIGE TVGRVLGIENQLFSWVLGLPESLRQVTVQSMREE IERSEVGDEGHHKLYPLKFRIILT LRYFHVQILLHRPILVKFLDATGPSGLEADEVKL LNDIGYSSMNKCVDSAMGIIDIIH ELVSTTGWQKDLLGAWWYSLYYTFNAALVIIGAM WVQRNRDTSEDPVDNGGNNNNMDI YLSRAVLTLQNLNVGNRMVDRCKYYLDQLITLLG LQADRIAETGIIISGMNPNVAGNST TGFDFPSLGIECGEFMIDDFPGFARGSGFERW"
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intron	18040..18107	/locus-tag="An18g01040"
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exon	18398..19163	/locus-tag="An18g01040"
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gene	complement(<20773..>22555)	/locus-tag="An18g01050"
mRNA	complement(join(<20773..21444,21501..21638,21710..22119,22180..22303,22370..>22555))	/locus-tag="An18g01050"
CDS	complement(join(20773..21444,21501..21638,21710..22119,22180..22303,22370..22555))	/locus-tag="An18g01050"

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 /inference="profile:PFAM:PF03055"
 /inference="similar to AA
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 /note="unnamed protein product;
 Catalytic activity:
 lignostilbene-alpha,beta-dioxygena
 se isozymes (LSD-I, II, and III)
 of P. paucimobilis catalyze the
 reaction
 1,2-bis(4-hydroxy-3-methoxyphenyl)
 ethylene + O(2) = 2 vanillin

Cofactor:
lignostilbene-alpha,beta-dioxygena
se isozymes (LSD-I, II, and III)
of *P. paucimobilis* require iron as
a cofactor. Complex: LSD-I, II,
and III consist of alpha
alpha,alpha beta, and beta beta
subunits, respectively. they show
different specificities for
several substrates that are
stilbene and styrene derivatives.
Function: LSD of *P. paucimobilis*
catalyses the oxidative cleavage
of the interphenyl double bond in
the synthetic substrate and
lignin-derived stilbenes. it is
responsible for the degradation of
a diarylpropane-type structure in
lignin. Similarity: the predicted
A. niger protein shows strong
similarity to subunit lsdB of
lignostilbene-alpha,beta-dioxygena
se isozyme LSD-III of *P.*
paucimobilis and related
dioxygenases from several plant
species. Title: strong similarity
to subunit lsdB of
lignostilbene-alpha,beta-dioxygena
se isozyme LSD-III -*Pseudomonas*
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GYEARGDGTDPVCYYTVGPDGKFT
EVLVWLVAPVAMIHDFAVTDNWWVIFPIIPQLCDI
ERMKQGGEHWQWSPETPLYLGVIP
RRGAKTADVKKWFQYKNSFPGHTANAHEDSSGNLI
IDLGLSEKNVFFWWPDAQGNAPEP
SSIRSQLVRFTINPRAEDLNLTEPRILQADNSEF
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		5-carboxymethyl-2-hydroxymuconate
		delta-isomerase from E. coli
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		5-carboxymethyl-2-hydroxymuconate
		= 5-carboxy-2-oxohept-3-enedioate.
		Pathway:
		5-carboxymethyl-2-hydroxymuconate
		delta-isomerase from E. coli is
		involved in tyrosine and
		phenylalanine metabolism.
		Similarity: the predicted A. niger
		protein shows strong similarity to
		5-carboxymethyl-2-hydroxymuconate
		delta-isomerase from E. coli and
		many putative
		2-hydroxyhepta-2,4-diene-1,
		7-dioate isomerases from several
		procaryotic and eucaryotic
		organisms. Title: strong
		similarity to
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		cytoplasm"
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		PFPFIFFKPNTCVHDHGEPVVIPRIAQNDQADYE

		VIGKDAKDVPVESALDYIAAYTVG NDISSRKLQRDPAYAGVVPQWGFSGGFDTFAPLG PVLVAASEIPDPSQLQLTTIVDGE VRQQESVGDLLFDCRYLISYLSQGTTLQKGSVIM TGTPGGKGKIFYC"
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exon	23443..23571	/locus-tag="An18g01060" /number=2
intron	23572..23666	/locus-tag="An18g01060" /number=2
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gene	<24984..>27426	/locus-tag="An18g01070"
mRNA	join(<24984..25058, 25166..25301, 25564..25745, 25812..26003, 26080..26144, 26206..26646, 26722..27303, 27423..>27426)	/locus-tag="An18g01070"
CDS	join(24984..25058, 25166..25301, 25564..25745, 25812..26003, 26080..26144, 26206..26646, 26722..27303, 27423..27426)	/locus-tag="An18g01070"

/inference="profile:COGS:COG0477"
/note="unnamed protein product;
Function: FLU1 of C. albicans facilitates resistance to fluconazole and cycloheximide in the fluconazole-hypersensitive S. cerevisiae strain YKKB-13 lacking the ABC (ATP-binding cassette) transporter gene PDR5. Function: FLU1 of C. albicans facilitates resistance to mycophenolic acid in C. albicans. Function: FLU1 of C. albicans is involved in the resistance to azol derivatives in C. albicans. Function: MDR1 of C. albicans facilitates resistance to the anti-mitotic drug benomyl and to the dihydrofolate reductase inhibitor methotrexate. Similarity: N-terminus of the A. niger protein is app. 120 aa shorter than in FLU1 of C. albicans. Similarity: the predicted A. niger protein shows strong similarity to fluconazole resistance protein FLU1 of C. albicans, which is a permease belonging to the major facilitator superfamily. Title: similarity to fluconazole resistance protein

FLU1 - Candida albicans"
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 MGGAGLSVAVPVLQQQLQRSQAEVTQLLTNLFLF
 LGIGNIFWVPLAVKFGKRASIISS
 MLLQAGALVWCAVATGYDSL LGARCVLGFAAAAG
 ESIVPEIVADIFFVHERATMMAIY
 VVLISGGSVAVGLIGGFVMEYASGTWRSYMWLCF
 ALASFNIVLLVFLFPESTFKRPEP
 SQAQELQLVAEHKETTSSFIENASAAAPEDSYTT
 NTPPFKGVLRPFHYNKDASFFKAV
 ISPLKLLVHPSVCWGIFTYGISLSPQIIMIFNFS
 ALLEASPYFFCSEYVGLMEIGAIV
 GFL LACYGGGYLSDIVNRMIAQRSSSSSIRPEQR
 LISLIPGMAIGPAGCILLAFACGH
 KLHWAIAVGF GMVSFGTVYTPNIALTYIVHLHQ
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CDS	complement(join(27797..28667))	/locus-tag="An18g01080"

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VMLRAYYYYPRVQEEYLLRLFLYRC
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CDS             join(28874..29683, /locus-tag="An18g01090"
29736..29875,
29925..30837)

/EC-number="3.1.1.5"
/inference="profile:PFAM:PF01735"
/note="unnamed protein product;
Catalytic activity:
lysophospholipase catalyses the
reaction 2-lysophosphatidylcholine
+ H(2)O = glycerophosphocholine +
a fatty acid anion. Pathway:
lysophospholipase is involved in
phospholipid degradation.
Similarity: the predicted A. niger

```

protein shows strong similarity to the protein sequences lysophospholipase (sequence 5 and sequence 7) of patents WO0127251-A/5 and WO0127251-A/7 from *A. oryzae* (AC# AX112082 and AC# AX112084) and to other fungal lysophospholipases. Title: strong similarity to lysophospholipase from patent WO0127251-A - *Aspergillus oryzae* extracellular/secretion proteins"

/citation=[14]
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/db-xref="GI:134084153"
/translation="MLSL LISAAAATLASALELP
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RDEAQWVEGRKNVILGSLDAYLKRLNLDDFDTDE
YISRLNNTSQTPIMGMAISGGGFG
SAYTGTGLIRALDDRLPAANEQRTGGLLQSM TYL
SGLSGGSWPAVSFPSYNFPTADEI
VDYWKPEIDRFFTVTNTSAEAATGKAIFEQIATK
YLAGFEVALSDYLGRGFAYEFIPG
QSGGLNTTFSGIRNLSNF INHQMPMPIIHLASVE
PEDAEYYDLLVPSSNGTIFDLTPF
EFGAWDGDVHAFTPTTEWLG NQLSNGIPVNQSKCW
KGFDRSSLVIGTSADAFNFWYLES
VSNGLTGQFAKRSTTHESSLTKRLSQPANLNALV
DAFQETFDLNL TQISYSKFPNPFT
NLSLSTGNTHKSSTLNLVDGSETGQTIPLWGQIQ
PARNVDFIIAWDDSQDADPYSWNN
GTNLYNTYLAANATGLPFPIIPPSRTMMNLNYTL
HPQFFGCDANLTTTGDDRAPIVLY
MANAPYSAYTNFSFWQTETSRQQMGEIFVNSFDI
VTQANGSWDGEWAECMGCAAVERS
LARVGMERTRQCQRCFERYCWDGTLDERDPGVLD
PTLVLDPGVKFGLWNATNPY"

sig-peptide	28874..28921	/locus-tag="An18g01090" /inference="protein motif:SignalP:2.0"
mat-peptide	join(28922..29683, 29736..29875, 29925..30834)	/locus-tag="An18g01090"
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exon	29736..29875	/locus-tag="An18g01090" /number=2
intron	29876..29924	/locus-tag="An18g01090" /number=2
exon	29925..30837	/locus-tag="An18g01090" /number=3
gene	complement(<30960..>32218)	/locus-tag="An18g01100"
mRNA	complement(join(<30960.. .31045,31081..31220, 31273..31630, 31702..>32218))	/locus-tag="An18g01100"
CDS	complement(join(30960..	/locus-tag="An18g01100"

31045,31081..31220,
31273..31630,
31702..32218))

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/inference="profile:COGS:COG1064"
/inference="profile:PFAM:PF00107"
/note="unnamed protein product;
Remark: the patent does not
provide further information about
the function of the protein.
Similarity: the predicted A. niger
protein shows strong similarity to
the protein sequence alcohol
dehydrogenase (sequence 19) of
patent EP0845532-A/19 from an
unclassified organism (AC# A92108)
and to other zinc-containing
dehydrogenases. Title: strong
similarity to alcohol
dehydrogenase from patent
EP0845532-A - Unclassified
organism cytoplasm"
/codon-start=1
/protein-id="CAK47187.1"
/db-xref="GI:134084154"
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GVIAVGEKVKT LAVGDRAAPITDT
EQITERATKRSWLA ADE DGV MADIYIVYDESVLCK
LPAYLDWVQASMIPCAGVTAWSAL
KGM RIGQTVLVQGTGGVSMFALKLALAAGLRVVL
TSSSDAKLQAIKEKYAGSAILTVN
YKNTPEWDEEVLKLTGGVGVDLVVENGGTGS
SLVK
SMRCTR RGGVVSQVGYLGKQDPSE
LSELVPTLIDRRINLRGINAGSKLDMEDFCEALS
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intron	complement(31631..31701	/locus-tag="An18g01100"
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		/number=3
exon	complement(31702..32218	/locus-tag="An18g01100"
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gene	<32976..>33236	/locus-tag="An18g01110"
mRNA	<32976..>33236	/locus-tag="An18g01110"

CDS	32976..33236	/locus-tag="An18g01110" /codon-start=1 /product="hypothetical protein" /protein-id="CAK47188.1" /db-xref="GI:134084155" /translation="MADQPPMGRDFIDAKNVDPV DHNDQTDPEDSASQPRFPGPGSSST TAPSTSKPHSNKLLNKLDPRYDSDVLESEKQENE KAQRREGWD"
exon	32976..33236	/locus-tag="An18g01110" /number=1
gene	complement(<33419..>35477)	/locus-tag="An18g01120"
mRNA	complement(join(<33419..33465,33522..34023,34080..34956,35015..35044,35095..>35477))	/locus-tag="An18g01120"
CDS	complement(join(33419..33465,33522..34023,34080..34956,35015..35044,35095..35477))	/locus-tag="An18g01120" /EC-number="1.-.-.-" /inference="profile:COGS:COG2303" /inference="profile:PFAM:PF00732" /inference="profile:PFAM:PF05199" /note="unnamed protein product; Catalytic activity: versicolorin B synthase from A. parasiticus catalyses the side chain cyclization of racemic versiconal hemiacetal to the bisfuran ring system of(-)-versicolorin B. Pathway: versicolorin B synthase from A. parasiticus is involved in the aflatoxin biosynthetic pathway. Remark: a splice site was detected upstream of the START codon. Remark: aflatoxins comprise a group of polyketide-derived carcinogenic mycotoxins. Remark: the genes encoding the aflatoxin biosynthetic enzymes in A. parasiticus are clustered. Remark: versicolorin B synthase from A. parasiticus possesses an amino-terminal sequence homologous to the ADP-binding region of other flavoenzymes, but does not require flavin or nicotinamide cofactors for its cyclase activity. Similarity: the predicted A. niger protein shows strong similarity to versicolorin B synthase from A. parasiticus and other oxidoreductases. Title: strong similarity to versicolorin B synthase vbs - Aspergillus parasiticus" /citation=[30] /codon-start=1

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                                GFVAENVPGANGRSIHYARGKCWGGSSAMNFMIIY
                                QRPTIESMEQWATAVNDSSYTFDQ
                                TLPFYKNSVKFTPPNTQIRAKNATAGYDPSAYES
                                TGGPLKVSYANYAMPFSTWMDLGM
                                KAIGINETQDFNLGSLMGGQYCASTIDPNGEVRS
                                SSEESFLANKPSTLTYYANTLAKK
                                IIFNNQKQATGVQVKGSAGNIYTIKANREVIVSA
                                GAFQSPQLLMVSGVGPQDQLEEHG
                                IQVVANRPGVGQNMWDHPFFAPSYRVNVQTFTAI
                                ANDFLGIVGQFINMVGFNGPLTN
                                PISDYLAWEKIPAALRSASFSSQTTKQLATFPSDW
                                PEAEYISGAGYMGVNSNLLINQPE
                                DGYQYASMLAVLITPTSRGNITLRSADTDDLPIVI
                                NPNWLATQSDQEVAIAMFKRVRAA
                                FQSKAMAPVIIIGNEYNPGLEVQSDEQILQWIKDN
                                VMTLWHAACCKMGTSDDEMAVVD
                                SQARVYGVQGVVVVDASAFPFLPPGHPQSTVYML
                                AEKIANEIIINGA"
sig-peptide      complement(35418..35477 /locus-tag="An18g01120"
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                                35015..35044,
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intron            complement(33466..33521 /locus-tag="An18g01120"
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exon              complement(33522..34023 /locus-tag="An18g01120"
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intron            complement(34024..34079 /locus-tag="An18g01120"
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exon              complement(34080..34956 /locus-tag="An18g01120"
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                                /number=4
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exon              complement(35095..35477 /locus-tag="An18g01120"
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                                /number=5
gene              <37406..>38455 /locus-tag="An18g01130"

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		/note="unnamed protein product;
		Remark: the patent does not
		provide further information about
		the function of the protein.
		Similarity: the predicted A. niger
		protein shows similarity to the
		protein fragment (SEQ ID NO:
		51484) of patent EP1033405-A2 from
		A. thaliana (AC# AAG41385) and to
		putative sterol desaturase family
		proteins. Title: similarity to
		protein fragment SEQ ID NO:51484
		from patent EP1033405-A2 -
		Arabidopsis thaliana"
		/codon-start=1
		/protein-id="CAK47190.1"
		/db-xref="GI:134084157"
		/translation="MSGTHPNPKDSMKSTWRRLD
		RAEWTIYHWFYEILGVHPEHLDKE
		VPVHQKTEKIPYMRTWSQHVVILYHAFIPLAVHH
		VYVSYTGQNFTPVGAFFFYIAFK
		LIAIHQLQVMRRMGHVLGFLDGDQHGDRGVPDVG
		VAKVVRSLISTSTFRPIMTVFLSY
		RVSQAPAQMSWGWLPLEIGLYGIILDFWFYWYHR
		LMHDVGSGLWKYHRTTHLTKHPNPL
		LTLYADTEQEFFDIAGIPLMTYFSMRLMGMPMGF
		YEWWICHQYVVFTELAGHSGLRMH
		ASPPSTLDWLLRLIGAELVIEDHDLHHRKGWKKS
		HNYGKQTRLWDKIFGTCHERIESR
		EGNVDYDNTVRMPIF"
exon	37406..38455	/locus-tag="An18g01130"
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gene	<38805..>39836	/locus-tag="An18g01140"
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		/inference="profile:PFAM:PF02558"
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		reductase -Salmonella typhimurium
		cytoplasm"
		/citation=[23]
		/citation=[42]
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		QHLIVAVKASATIPALRSIQHRLG
		RHSVICLFQNLGQIEELNERLFTDPLTRPTYMF
		GIMRHGVYIKAPFEAVLAGLTGSC
		ALGIVNNDQQASSLSASSTASQSRFLINRLVEA
		PIVRSSSELPWMELHQAQLLKLATN
		CVVNPLTALLDVRNGSLLANSELQEMRRQLLQEI
		SLVFRRLPEFQGLPDVEEQFSVAR
		LEEQLIGNIEKTASNSSMREDVRAGRATEIAYI
		NGWIVRRGQQLGLDCPTNRCLTQL

sig-peptide	38805..38876	ILAKSSQGR" /locus-tag="An18g01140" /inference="protein motif:SignalP:2.0"
mat-peptide	38877..39833	/locus-tag="An18g01140" /product="unnamed"
exon	38805..39836	/locus-tag="An18g01140" /number=1
gene	<40728..>42671	/locus-tag="An18g01150"
mRNA	join(<40728..41152, 41226..42344, 42401..>42671)	/locus-tag="An18g01150"
CDS	join(40728..41152, 41226..42344, 42401..42671)	/locus-tag="An18g01150" /inference="profile:COGS:COG0477" /inference="similar to AA sequence:UniProtKB:AF188621.1" /note="unnamed protein product; Function: FLU1 of C. albicans facilitates resistance to fluconazole and cycloheximide in the fluconazole-hypersensitive S. cerevisiae strain YKKB-13 lacking the ABC (ATP-binding cassette) transporter gene PDR5. Function: FLU1 of C. albicans facilitates resistance to mycophenolic acid in C. albicans. Function: FLU1 of C. albicans is involved in the resistance to azol derivatives in C. albicans. Function: MDR1 of C. albicans facilitates resistance to the anti-mitotic drug benomyl and to the dihydrofolate reductase inhibitor methotrexate. Similarity: the predicted A. niger protein shows strong similarity to fluconazole resistance protein FLU1 of C. albicans, which is a permease belonging to the major facilitator superfamily. Title: strong similarity to fluconazole resistance protein FLU1 - Candida albicans" /citation=[59] /codon-start=1 /protein-id="CAK47192.1" /db-xref="GI:134084159" /translation="MSPIDEQLEMAEVDARPHTN GASKEEGLERPSSSGTTGSTGYSS SLEYNPQLHTLHSRNTELDLERHRTATSHALSRI ETQRLQHQLTVGESVKSRASRTPL PRMGANKDYPPLPDREDYVVEFDGPDPLYPQN WELGTKIYISAILAFTSICSTFDS AIFSSSTTNVARVFGVGIEVATLSSSLYICGYAS GPLVWAPLSELKGRKPPIVVAMLG FGIFNTAVAVAKDLQTIMICRFFCGVFGSCPLAV VAAVFSDIYNNRTRGVAIAMFSST VFLGPLLAPFIGGFINTSYLGWRWTAYIPAFMGY AAFVLNMFFLKESYPPIILVSKAS ELRRRTKNWGIHAKQEEIEVDLRELLVNNFSRPL

		RLLFGEPLILAVTIYLSFIYGLLY CFLTAYTLVFQGVYGMSAGVGGLTLFGMVVGLFI AASYIIFASRGYNKKLEANGGIPV PEWRLPPVIIGGALFAGGLFWFGWTGFTKSIHWI VPTLSGLFTGLGLLIIFIQLFNLY IDTYLMFAASAIAANTFCRSLVAASFPLFSRQMF NNMGIQWAATLLGCVASILVPIPV AFYFYGKNLRKRSKFAPFYDKVAESHAEDPVENG VAEH"
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intron	41153..41225	/locus-tag="An18g01150" /number=1
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intron	42345..42400	/locus-tag="An18g01150" /number=2
exon	42401..42671	/locus-tag="An18g01150" /number=3
gene	42950..43033	/gene="tRNA-His (GTG)" /locus-tag="An18e01160"
tRNA	42950..43033	/gene="tRNA-His (GTG)" /locus-tag="An18e01160" /product="tRNA-His" /inference="profile:tRNAscan:1.4" /note="codon recognized: CAC"
gene	<43783..>45994	/locus-tag="An18g01170"
mRNA	join(<43783..43852, 43912..44025, 44075..44344, 44395..45240, 45294..45376, 45425..>45994)	/locus-tag="An18g01170"
CDS	join(43783..43852, 43912..44025, 44075..44344, 44395..45240, 45294..45376, 45425..45994)	/locus-tag="An18g01170"

/EC-number="2.4.2.30"
/inference="profile:PFAM:PF00644"
/inference="profile:PFAM:PF02877"
/note="unnamed protein product;
Catalytic activity: the NAP
protein of Z. mays catalyses the
reaction NAD(+) +
{ADP-D-ribosyl}(N)-acceptor <=>
nicotinamide +
{ADP-D-ribosyl}(N+1)-acceptor.
Function: the NAP protein of Z.
mays is involved in programmed
cell death or apoptosis.
Localization: the NAP protein of
Z. mays is a nuclear enzyme.
Remark: the ADP-D-ribosyl group of
NAD(+) is transferred to an
acceptor carboxyl group on a
histone or the enzyme itself, and
further ADP-ribosyl groups are
transferred to the 2'-position of
the terminal adenosine moiety,
building up a polymer with an

average chain length of 20-30 units. Remark: the NAP polynucleotide sequences can be used for modulation of programmed cell death in eukaryotic cells. the method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc. , or during transformation). particular applications are generation of plants that are resistant to fungi or nematodes; are male or female sterile ; or have better seed-shatter properties. the methods are also used to improve growth of transformed plant cells (and derived calli or complete plants). Similarity: the predicted A. niger protein shows strong similarity to the protein sequence poly(ADP-ribose) polymerase NAP protein of patent WO200004173-A1 from Z. mays (AC# AAY68834) and from many other eucaryotic organisms. Title: strong similarity to poly(ADP-ribose) polymerase NAP protein from patent WO200004173-A1 - Zea mays nucleus"

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DDEPESPKKRTLEQALGINEDGTTKKLKDAQTVG
TKQINVPVDDTCPLRLTFTVYIDP
TG LIWDATLNQTSATNNNNKFYRIQLLHRNNEFR
TWHWGRVGEHGQHALLGGGGLDE
AEYEFKKKFKDKSGLTWENRLDPPKKGKYTFIEK
NYEEDTEDEDEDEKVVAKKPTKP
KAEEVKCTL SAPVQDLVSFIFNKDFQSTMASMS
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		SWGSGNRGLLLLLCDVEVGNPMYER
		DTASFNAGQEAKAEAKIATLGRGRSIPGGWKDAG
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		/EC-number="3.5.1.11"
		/note="unnamed protein product;
		Function: penicillin V
		amidohydrolase (PVA) from F.
		oxysporum is used for the
		enzymatic hydrolysis of penicillin
		V (phenoxy-methylpenicillin) to
		6-aminopenicillanic acid (6-APA).
		6-APA is the active beta-lactam
		nucleus used in the manufacture of
		semi-synthetic penicillins.
		Similarity: the predicted A. niger
		protein shows strong similarity to
		the protein sequence penicillin V
		amidohydrolase (PVA) of patent
		US5516679-A from F. oxysporum (AC#
		AAW00291). Title: strong
		similarity to penicillin V
		amidohydrolase PVA from patent
		US5516679-A - Fusarium oxysporum
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		GGLAAGIIGLAPAHFVSQGYATAATDGGLTLNGT

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intron	48455..48517	/locus-tag="An18g01180"
		/number=1
exon	48518..48537	/locus-tag="An18g01180"
		/number=2
gene	complement(48889..48960)	/gene="tRNA-Ala (AGC) "
		/locus-tag="An18e01190"
tRNA	complement(48889..48960)	/gene="tRNA-Ala (AGC) "
		/locus-tag="An18e01190"
		/product="tRNA-Ala"
		/inference="profile:tRNAscan:1.4"
		/note="codon recognized: GCU"
gene	<49850..>51919	/locus-tag="An18g01200"
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CDS	join(49850..49888, 49981..50173, 50233..50362, 50419..50614, 50702..50828, 50883..51127, 51199..51470, 51538..51919)	/locus-tag="An18g01200"
		/EC-number="1.14.-.-"
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		/inference="profile:PFAM:PF00067"
		/inference="similar to AA sequence:UniProtKB:AFU81806.1"
		/note="unnamed protein product; Function: ord1 of A. flavus converts O-methylsterigmatocystin to aflatoxin B1. Pathway: ord1 of A. flavus catalyzes the last step of the aflatoxin biosynthetic pathway. Remark: aflatoxins comprise a group of polyketide-derived carcinogenic mycotoxins. Similarity: the predicted A. niger protein shows

strong similarity to
O-methylsterigmatocystin
(OMST)-oxidoreductase (ord1) from
A. flavus, which belongs to the
CYP64 family of cytochrome
P450-type monooxygenases. Title:
strong similarity to
O-methylsterigmatocystin
oxidoreductase ord1 - Aspergillus
flavus"

/citation=[36]

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LESRSSIHSSRPQQHFAEMAGWNNVNLGAVKQSQR

FRATRKNLHREIGSNVSVARFNEI

QTAEVGRFLLRVLDAPDKLMKHIRKWWGYGYTIE

PHDQDPLVDLADKAMMDFSMAMLP

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GSSVLANIWAFTHDPAAYHDPMTFKPERFLSPKP

ERDPHFLVFGFGRRVCPGRTLADV

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exon 50883..51127

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intron 51471..51537

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/number=7

exon 51538..51919

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           52635..52939,
           52984..53309,
           53368..>53720))
CDS        complement(join(52148.. /locus-tag="An18g01210"
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           52984..53309,
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           /inference="profile:PFAM:PF00069"
           /note="unnamed protein product;
           Function: SRPK2 from M. musculus
           phosphorylates SF2/ASF, a member
           of SR splicing factors. Remark:
           overexpression of murine SRPK2
           causes disassembly of
           cotransfected SF2/ASF and
           endogenous SC35. SRPK family
           members may regulate the
           disassembly of the SR proteins in
           a tissue-specific manner.
           Similarity: the predicted A. niger
           protein shows similarity to SRPK2
           from M. musculus and strong
           similarity to putative
           serine/threonine protein kinases
           from several eucaryotic organisms.
           Title: similarity to
           SR-protein-specific kinase SRPK2 -
           Mus musculus nucleus"
           /citation=[39]
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           LGYGVSTVWLGRDLRDSKYVVLKIYVTGQEKNH
           ELEIYNRMNAVEVEHPGRDLVRRL
           FDHFTVTGPHGPHVCLVHEPMGMSADTLLQKYIP
           GNTMTLDEMKTICIRQLLIALDFLH
           SAARIVHTGKDLQLKNLLLPVPNTKTLETLEERE
           VNDPSPRKILKDRTIYLSTVYNPG
           GSGLPLISDFGEARFGDVEKRDDIMPNNMYRAPEV
           VLKENWNYKVDIWNVAMVAWDIVI
           PRHMF DGRNADGIFDDR VHIAEMIALMGPPPASF
           RERCRLAYVFWDEQGNWKDLAPIP
           DISLES LGADIPGENREGFFRWLRKALQWNAEDR
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55559..>55762))
CDS complement(join(54105.. /locus-tag="An18g01220"
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55392..55500,
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sequence:PIR:S64826"
/note="unnamed protein product;
Function: in S. cerevisiae,
mutants (dal5) that lack
allantoate transport have been
isolated. these strains also
exhibit a 60% loss of allantoin
transport capability. Regulation:
in S. cerevisiae Dal5 appears to
be sensitive to nitrogen
catabolite repression, feedback
inhibition, and trans-inhibition.
Regulation: in S. cerevisiae
allantoate uptake is constitutive.
Similarity: the predicted A. niger
protein shows strong similarity to
allantoate permease gene (DAL5)
from S. cerevisiae, which belongs
to the major facilitator
superfamily. Title: strong
similarity to allantoate permease
Dal5 - Saccharomyces cerevisiae"
/citation=[7]
/citation=[9]
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 GFQHVHHGATLAGWRIMFLVIGLV
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 SVNQTGVWSSAINLKQIWEGVLDI
 QLWLLVLITILISVSSGVVTTYATLIAGFGYSG
 PISALLNMPSGIVSIFFTLLVGFG
 IRRTSRWAUNAFACTIPGIIIGGLLSFLPKSNKA
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mRNA	join(<56384..56645, 56694..56761, 56818..57009, 57069..57368, 57430..57711, 57897..58158, 58326..>58444)	/locus-tag="An18g01230"
CDS	join(56384..56645, 56694..56761, 56818..57009, 57069..57368, 57430..57711, 57897..58158, 58326..58444)	/locus-tag="An18g01230"

/note="unnamed protein product;
 Function: M. grisea Pth11 is a
 pathogenicity gene. Function: M.
 grisea Pth11p likely is involved
 in host surface recognition.
 Function: M. grisea pth11 mutants
 of strain 4091-5-8 are
 nonpathogenic due to a defect in
 appressorium differentiation.
 Localization: in M. grisea, a
 Pth11-green fluorescent protein

fusion localised to the cell membrane and vacuoles. Similarity: similarity of the predicted A. niger protein and M. grisea Pth11 is limited to the N-terminal half of the protein sequences. Title: similarity to integral membrane protein PTH11 - Magnaporthe grisea plasma membrane"

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ADLPDYTKLNYAGRPFYQLGIAGFKASLCLNYLR
LISGTSKNFYRILIWAVIAVSTLG
HLAGTLVLIFDCQPVERAWNPNISGSCLPAGPTF
YGLAIFTIICDITIIILPIPLLLQ
LNIKTAQKAGVVCLFLLGLFTTICSILRLTQIHR
VAYGDGNSTMLVLWGTIEFNVGNI
VTCVPFLAPLLKGAVRDFRSYSGRKGYSRSYAL
QTWSKDPsQLRSTTSAAPQPKRT
PSEELILESGGVDEGGIHMTVELRVsLEKRPTTE
HDGINSAYASQDQIRPGSYWVDVT
DTSQWSRAEQARPTVPDGIFPAIKPSSIQEESCA
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CDS	60374..>60560) join(59070..59441, 59521..59806, 59879..60178, 60237..60312, 60374..60560)	/locus-tag="An18g01240" /inference="profile:COGS:COG0654" /inference="profile:PFAM:PF01360" /note="unnamed protein product; Catalytic activity: NahW of P. stutzeri catalyzes the conversion salicylate + NADH + O(2) <=> catechol + NAD(+) + H(2)O + CO(2). Pathway: NahW of P. stutzeri is involved in the metabolization of naphtalene and salicylates (lower naphtalene degradation pathway). Similarity: the predicted A. niger protein shows similarity to salicylate hydroxylase (nahW) of P. stutzeri, which belongs to the NADH-dependent monooxygenase superfamily. Title: similarity to salicylate hydroxylase nahW -Pseudomonas stutzeri" /citation=[51] /codon-start=1 /protein-id="CAK47199.1" /db-xref="GI:134084166" /translation="MDDLPLVLIWGAGISGLLLAQ HLQKLGVPYKIFERDAAIDARSGG WGLTLHWALPALRELLPDHLVQRLPEAYVNKAAA ARGDTGRFSFFDLKTGSALYSVPA AERIRVSRVRLRQLVATGLDVQWNKTLQNIESTA DTVTAHFADGTSYTGCLLIGCDGS RSPTREILYPDSHEMNPLPVQILGAATLYTAEEM AGAAEIDPFIFQGSHPESNVFLFF SILDTPNNFVESSKDKYECQIILSWADSKDIAVP SDNGERIALMKSLASDWAEPFRTL VHRLSEDTEARSIRIADWMFRPLQNRSHPRVVL GDSAHTMTMYRGEGANNAIVDVLD LTQRVDMRSLGTMSTQALRDALDAYENDVFRRAE PSVLNSRQACVDAHDFTRILDESP LVSARVLKEDTTEQ"
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gene	complement(61713..61825)	/number=2 /gene="tRNA-Leu (CAG)"
tRNA	complement(61713..61825)	/locus-tag="An18e01260" /gene="tRNA-Leu (CAG)"
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		YPAVAWCWMTPKYESMRLWTHYFW
		IFASEFFTIVVLYAIMFIQLRKKIAESAILGEHNS
		ESLTRLKRVIFHMALYPVVIICLT
		LPLAAGRMASASGHSPSVLYFCFAGSFMTLCGFC
		DSLMYTLSRRSVVLEPEARIHGSS
		NKYSSRPNKSSVAHHYGN SIDGKGPTNTTIARGR
		SDSTEEMIGKDGLELAPMGVVLQH
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		/note="unnamed protein product;
		Remark: paiB from B. subtilis
		seems to be essential. Similarity:
		the predicted A. niger protein
		shows weak similarity to
		transcription regulator 2 of the
		pai operon of B. subtilis and
		conserved hypothetical proteins
		from several procaryotic
		organisms. Title: similarity to
		transcription regulator paiB
		-Bacillus subtilis"
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		HSYITPHFYTTTKPLTGKVAPTWNYYAAVQVYGRA
		RIYNPRSEGELGEQASMFLDTQLR
		DLTAHCEGEIMGYTTTGTSDTYTHNNPEEKSCPR
		AWTVDEAPDAYINILKKNIIGIEV
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/EC-number="3.4.23.35"
 /inference="profile:PFAM:PF00026"
 /note="unnamed protein product;
 Function: BAR1 of *S. cerevisiae*
 selectively cleaves the
 6-Leu-|-Lys-7 bond in the
 pheromone alpha-mating factor.
 BAR1 activity is abolished by in
 vitro mutation of an aspartic acid
 predicted to be in the active
 site. Induction: secretion of BAR1
 of *S. cerevisiae* is stimulated to
 as much as five times the basal
 level by exposure of cells to
 alpha-factor. Localization: BAR1
 of *S. cerevisiae* is secreted into
 the periplasmic space of MATa
 cells. Remark: BAR1 of *S.*
cerevisiae is already active in
 early compartments of the
 secretory pathway. Bar1 protease
 tolerates large N-terminal
 extensions of its substrate and
 does not require Golgi-specific
 modifications such as outer-chain
 glycosylation for activity.
 Remark: the protein sequence of
 barrier protease BAR1 of *S.*
cerevisiae is covered by patent
 WO9118988-A (AC# AAR20109). the
 patented barrier protease is
 useful in industrial processes
 where leucine-lysine or
 leucine-arginine cleavage is
 required at low pH or high
 temperature. barrier protease may
 also be used in the production and
 isolation of proteins made by
 genetic engineering methods, e. g.
 to cleave fusion proteins at
 Leu-Arg bonds. Similarity: the
 predicted *A. niger* protein shows
 strong similarity to extracellular
 protease precursor BAR1 of *S.*
cerevisiae which belongs to the
 subfamily A1 of aspartic-type
 peptidases. Title: strong
 similarity to extracellular
 protease precursor Bar1 -
Saccharomyces cerevisiae
 extracellular/secretion proteins"
 /citation=[2]
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		/inference="profile:PFAM:PF00328"
		/note="unnamed protein product;
		Remark: the patent does not
		provide further information about
		the function of the protein,
		except for a claim of phytase
		activity. Similarity: the
		predicted A. niger protein shows
		strong similarity to protein
		sequence 11 from patent
		EP0684313-A/11 and several
		putative phytases. Title: strong
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		organism"
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mRNA	complement(join(<77988.. .78215,78264..78441, 78499..79055, 79113..79172, 79229..79241, 79298..79508, 79560..79700, 79753..>79819))	/locus-tag="An18g01350"
CDS	complement(join(77988.. 78215,78264..78441, 78499..79055, 79113..79172, 79229..79241, 79298..79508, 79560..79700, 79753..79819))	/locus-tag="An18g01350" /inference="profile:COGS:COG2141" /note="unnamed protein product; Remark: HA protein regulates homeostasis and adaptation. the C. glutamicum HA genes (I) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polyketide or enzyme. the amino acids produced can be lysine, glutamine, glutamate,alanine, aspartate, glycine, serine, threonine, methionine,cysteine, valine, leucine, isoleucine, arginine, proline,histidine, tyrosine, phenylalanine, or tryptophan. the fine chemical production can be modulated. the presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynebacterium

diphtheriae. (I) can be used to map the *C. glutamicum* genome or can be used as markers for genetically engineered *Corynebacterium* or *Brevibacterium*. the HA proteins encoded by the (I) are used to maintain homeostasis in *C. glutamicum* or help the microorganism to adapt to different environmental conditions. Similarity: the predicted *A. niger* protein shows strong similarity to HA protein sequence SEQ ID NO:420 from patent WO200100842-A2 (AC# AAB79232), which is a monooxygenase by similarity. Title: strong similarity to HA protein sequence SEQ ID NO:420 from patent WO200100842-A2 - *Corynebacterium glutamicum*"

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QQPQHDDRYAQAE EYIKVTYKLWESSWRSDAVVL
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ATVGQHITVGG LGATPVGTPEQVA
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 /note="unnamed protein product;
 Function: S. cerevisiae DUR3 is a
 urea symporter mediating urea
 import. Induction: high-level
 expression of S. cerevisiae DUR3
 is inducer dependent, requiring
 functional DAL81 and DAL82 genes.
 Regulation: expression of S.
 cerevisiae DUR3 is regulated in a

manner similar to that of other genes in the allantoin pathway. Repression: DUR3 expression is highly sensitive to nitrogen catabolite repression and also has a partial requirement for the GLN3 product. Repression: maintenance of *S. cerevisiae* DUR3 mRNA at uninduced, nonrepressed basal levels requires the negatively acting DAL80 gene product. Similarity: *S. cerevisiae* DUR3 belongs to the major facilitator family. Title: strong similarity to urea transport protein Dur3 - *Saccharomyces cerevisiae* plasma membrane"

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ACANMLLGAAAVISAITGMHIIAATFLLPVGVTV
YTFVGGIKATFLTDYFHTAILII
ACYLSVKAFTFEEVGSIGKLYELVQAAAQRHPVS
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SNFGLVIMDTSYFIKAFSAAPSSVVPGYTIGGIA
YFAIPWALGTIMSSLALGLENTAS
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VWLGT AQHFYGA VSVSSTGQILPC
VYGTVASAFSPIVYSVLITLVKPQRYDWAEFRKE
KLGLERLDS DSDITVNGQGSEEQQ
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exon	84864..85018	/number=5 /locus-tag="An18g01370"
gene	complement(<85096..>90863)	/number=6 /locus-tag="An18g01380"
mRNA	complement(join(<85096..85140,85234..85322,85463..86109,86186..86269,86334..86527,86604..87025,87079..87143,87317..87548,87617..87964,88032..88194,88244..88541,88598..89091,89221..89335,89500..90057,90157..90274,90374..90575,90645..>90863))	/locus-tag="An18g01380"
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Remark: mutagenesis experiments demonstrate that conserved amino acid residues, functionally critical in the human cystic fibrosis transmembrane conductance regulator (hCFTR), play a vital role in YCF1-mediated cadmium resistance. Remark: substitution of a serine to alanine residue in a potential protein kinase A phosphorylation site in a central region of YCF1, which displays sequence similarity to the central regulatory domain of hCFTR, also rendered YCF1 nonfunctional.

Remark: the YCF1 gene of *S. cerevisiae* is an MgATP-energized, uncoupler-insensitive vacuolar membrane glutathione S-conjugate transporter. Similarity: the predicted *A. niger* protein shows strong similarity to cadmium factor (YCF1) from *S. cerevisiae*, which belongs to the ATP binding cassette (ABC) protein superfamily of membrane transporters. Title: strong similarity to cadmium resistance protein Ycf1 - *Saccharomyces cerevisiae* [putative sequencing error] putative sequencing error"

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	/number=16
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mRNA      complement(<91484..>93088) /locus-tag="An18g01390"
CDS       complement(91484..93088) /locus-tag="An18g01390"
)
/inference="profile:PFAM:PF00046"
/note="unnamed protein product;
Function: the CUP1 gene, and its
copper-dependent transcriptional
activator ACE1 play a key role in
mediating copper resistance in S.
cerevisiae. Similarity: the
predicted A. niger protein shows
similarity to the copper
homeostasis protein CUP9 from S.
cerevisiae. the predicted A. niger
protein shows strong similarity to
the homeobox domain of many
homeotic proteins. Title:
similarity to copper homeostasis
protein Cup9 - Saccharomyces
cerevisiae nucleus"
/citation=[26]
/codon-start=1
/protein-id="CAK47212.1"
/db-xref="GI:134084179"
/translation="MEHAHQAFPKLCDDILSLPP
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DELAQRTSLTRAQVSNWFINARRRKRSSGYMSAR
QSPSFLSPMERWRSSPPESEAAAT
DDILRALADSDISAFSDSLPYTPVQYAWSSNDSS
GSFVLGDASISSCGRSQSSSSEKS
VALSSHRPPQRPPTPLHRPSSRRHRKHIRHANR
LQWTRRPYQCTFCADTFATKYDWQ
RHEKALHLPVDQWRCSPGGGLIIDNNGTPVCVFC
QQANADEDHLETAHNYSTCLEKPS
EQRIFTRKDNLRQHLKLTHRVDTFHAAMLTWRES
RGHRILSRCGFCSATFQSWQERVD
HVAEHFKHGADMKQWMGDWGFEPQAQRLVENAIP
PYLIGREAQTPDPWRTSDVFPMPR
EEDKEDDEIPFRWDVPTALDRYFDVHRDLLAFIR
EQMSNGCRPSDQMIQDRARLFAYE
SDDPWNQTYADDLCWLEAVKQEAGLV"

exon      complement(91484..93088) /locus-tag="An18g01390"
)

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mRNA      join(<93571..93941, /locus-tag="An18g01400"
93988..94242,
94300..94738,
94796..>94963)
CDS       join(93571..93941, /locus-tag="An18g01400"
93988..94242,
94300..94738,
94796..94963)

/inference="profile:COGS:COG0477"
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/note="unnamed protein product;

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Function: the MCT3 transporter from *Rattus norvegicus* is a proton-linked monocarboxylate transporter. it catalyzes the rapid transport across the plasma membrane of many monocarboxylates such as lactate, pyruvate, branched-chain oxo acids derived from leucine, valine and isoleucine, and the ketone bodies acetoacetate, beta-hydroxybutyrate and acetate. Similarity: the predicted *A. niger* protein shows strong similarity to the monocarboxylate transporter 3 (MCT3) of *R. norvegicus*, which belongs to the major facilitator superfamily. Title: strong similarity to monocarboxylate transporter 3 MCT3 - *Rattus norvegicus*"

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YFKAKRGIANGIVYAAGGLGGAII
SFILDALLSRVGTAWTFRILGFITMGTGLPAAFL
VKQRIPIPPSAFVEWRLFRDIRFL
LLFAAGAIATFPLLVPFFFLPLYTDSLGLGSAAG
AGVVAAFNFSSALGRLTCGFASDT
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VIINGMANGGFFSTIPTVVGNVFG
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intron	93942..93987	/locus-tag="An18g01400" /number=1
exon	93988..94242	/locus-tag="An18g01400" /number=2
intron	94243..94299	/locus-tag="An18g01400" /number=2
exon	94300..94738	/locus-tag="An18g01400" /number=3
intron	94739..94795	/locus-tag="An18g01400" /number=3
exon	94796..94963	/locus-tag="An18g01400" /number=4
gene	<95725..>97215	/locus-tag="An18g01410"
mRNA	join(<95725..95803, 95882..96591, 96649..>97215)	/locus-tag="An18g01410"
CDS	join(95725..95803, 95882..96591, 96649..97215)	/locus-tag="An18g01410"

		/inference="profile:PFAM:PF03663" /inference="similar to AA sequence:PIR:T52516" /note="unnamed protein product; Title: strong similarity to hypothetical protein B2J23.120 - Neurospora crassa" /codon-start=1 /protein-id="CAK47214.1" /db-xref="GI:134084181" /translation="MLLRIWHILYTFIVVVQAID YDVDDPDSIKAACHSVARQMLTHY TGNQPGDNPGNLPDPYYWWEAGAMFTALVDYWYL TSDDTWNNITTQGITWQAGPSGSF MPANQTRTEGNDDQSFWAFAAMSAAERNFPDPPP SSGSPGWLAMAQAVFNTQAARWDK STCNGGLRWQIFTFNNGWTYKNTISNGCFFNLAA RLAKYTG NSTYADWADTVVDWTGE VGFMTDTYRFWDGADVSSGCGDWNYYIEWTYNTGV YLLGAAVMYNLTESPVWKARTEGI LNASFVFFQDDVMYERACEPVSTCQVDQRSFKGY LARWMAATTQMAPFTYDLVMPKLR ASAKAAAETCTGGELQATCGLKWTDRKWDGMDDV GIQMAALEVMQSTLISRVDPPVTQ DTGGTSQGNPAGGEPGPPAPVPEGLRLEITKAD RAGAGMMTVMLSMIVIGSTGWMVY E" /locus-tag="An18g01410" /inference="protein motif:SignalP:2.0" /locus-tag="An18g01410"
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mat-peptide	join(95779..95803, 95882..96591, 96649..97212)	
exon	95725..95803	/product="unnamed" /locus-tag="An18g01410"
intron	95804..95881	/number=1 /locus-tag="An18g01410"
exon	95882..96591	/number=1 /locus-tag="An18g01410"
intron	96592..96648	/number=2 /locus-tag="An18g01410"
exon	96649..97215	/number=2 /locus-tag="An18g01410"
gene	complement(<97301..>989	/number=3 /locus-tag="An18g01410"
mRNA	81) complement(join(<97301. .98523,98588..>98981))	/locus-tag="An18g01420"
CDS	complement(join(97301.. 98523,98588..98981))	/locus-tag="An18g01420"
		/codon-start=1 /product="hypothetical protein" /protein-id="CAK47215.1" /db-xref="GI:134084182" /translation="MVRGRPRPSRFTRTSPSCAS GTTRMCRNRRPLQARRVMQVYSNL TCSYPIPTIMPALSVLPADILLHVISFLDHSGDV YSFSLLSPSLFTLIHSNDLVNKTR YRCVRINCTPDLKNAYTILLDILHDCNLANMIAL LTQATCSVSVRPPPGPALSVRNRR DYSTWPCRRQTTLRIGSISHTTSAFSITVIEITT VSNPASTQEDAYHGKSTFIGQALT VLLIASSPNLTSLAISPPFWEYTSSRFNDPSDNH

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HFAAKIEKYPLAKFLKHANSSHLI
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GGCYAGFAEFFDRYSLIEAILRHRATLEVLDFEF
DDQLSQFVAVERESGVQDDAEDKS
VLKEFISLRSLSLGVSCWFLATGMGELGNIVLM
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/inference="profile:PFAM:PF00107"
/inference="similar to AA
sequence:PIR:S45605"
/note="unnamed protein product;
Catalytic activity: alcohol + NAD+
= aldehyde or ketone + NADH.
Pathway: alcohol dehydrogenase
ADH-T from B. stearothermophilus
is involved in glycolysis /
gluconeogenesis; fatty acid
metabolism; bile acid
biosynthesis; tyrosine metabolism;
glycerolipid metabolism. Remark:
the protein sequence of alcohol
dehydrogenase ADH-T from B.
stearothermophilus NCA1503 is
covered by patent JP04218378-A
(AC# AAR26874). Similarity: the
predicted A. niger protein shows
strong similarity to thermostable
alcohol dehydrogenase ADH-T from
B. stearothermophilus NCA1503,
which belongs to the zinc alcohol
dehydrogenase (ADH) family. Title:
strong similarity to thermostable
alcohol dehydrogenase adhT -
Bacillus stearothermophilus"
/citation=[15]
/citation=[58]
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intron	complement(101142..101213)	/locus-tag="An18g01430"
		/number=1
exon	complement(101214..101496)	/locus-tag="An18g01430"
		/number=2
gene	<101875..>104542	/locus-tag="An18g01440"
mRNA	join(<101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..>104542)	/locus-tag="An18g01440"
CDS	join(101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..104542)	/locus-tag="An18g01440"
		/inference="profile:COGS:COG3496" /note="unnamed protein product; Similarity: the predicted A. niger protein shows local similarity to the hypothetical protein mll8086 from M. loti. Title: strong similarity to hypothetical protein CAD70872.1 - Neurospora crassa" /codon-start=1 /protein-id="CAK47217.1" /db-xref="GI:134084184" /translation="MTAKCMVIKKAEDHTEFLG LHHVGSCKNFDCVTKVGRGPQIL KKFLLRQWIPAQGGREQQPESLILSPVRKNLPSI SVDGILLHAALLTVNLILKLGGWP GLLKFMLRTFAISSVLAPIGLIGFLVLSFTPRN IKSLSKDKSVIGKPLLFPITLDHT RLSPIKNNFTFNVLFVGIPVGISCRFGRLLSIDA KHTDEEECTERSLLRLLQTYFSS WFSFDSARYLHRGDDTLLENKLNKFLREQNENP AKWPYAYMLSVPRFLWWERSVVTW WYLYSESKELDAVIMEINNSFDEKRNVLKVRRT RIYTESPEKGFEQLLDCKEEHLDE DKRVFSLIPQHGKYAYKATWKKEIFSSPFKEKVG TVSSTFLDPVVPSSWSGNRSLSNT TTFDPSGAPRMIALRWCKVPPIDPGKASSFQIFS ILLIWTNVNLTATPRILFQAIRLH VMNLMRMEHPDVRPGSEPRRPSKGERKDAPLKM LHSLFDLHANLQSRMLERFFREYL

		KHIVASYPGDLEVITYIPCKSVFKTTICLRSTQYS AEGQDPRRLRLEVMDPAFYSRIVN SPNAGTAMAKETKPGRSPADALSSPVIASDITQS LQLLDVTVSENRTYDKACSRISW VLCLRRWLTSSFMDSFVCKALPPRTQEEYVSCLI QLWLEKLTWDFLSPHQIYRVIRAA MLQWAICWILF"
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		/number=2
intron	102220..102258	/locus-tag="An18g01440"
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intron	102361..102391	/locus-tag="An18g01440"
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exon	102392..102399	/locus-tag="An18g01440"
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gene	<106231..>106803	/locus-tag="An18g01450"
mRNA	join(<106231..106565, 106647..>106803)	/locus-tag="An18g01450"
CDS	join(106231..106565, 106647..106803)	/locus-tag="An18g01450"

/EC-number="1.14.-.-"
 /note="unnamed protein product;
 Function: ordA of A. parasiticus
 is involved in the aflatoxin
 biosynthesis and converts
 O-methylsterigmatocystin (OMST) to
 aflatoxins B1 or G1 and converts
 dihydro-O-methylsterigmatocystin
 (DHOMST) to aflatoxins B2 or G2.
 Remark: aflatoxins comprise a
 group of polyketide-derived
 carcinogenic mycotoxins. Remark:
 it is assumed that the ORF is
 N-terminally shorter and has
 another start codon 5' to the
 predicted one ; the ORF is around
 400 amino acids shorter than most
 of the homologues cytochrome p450
 proteins. Remark: ordA of A.
 parasiticus is also called
 cytochrome p450 64, cyp64 or omst
 oxidoreductase. Similarity: the
 ORF shows similarity to several
 cytochrome P450 related proteins
 from different species. Title:
 strong similarity to
 O-methylsterigmatocystin
 oxidoreductase ordA - Aspergillus

		parasiticus"
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		/protein-id="CAK47218.1"
		/db-xref="GI:134084185"
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exon	106231..106565	/locus-tag="An18g01450"
		/number=1
intron	106566..106646	/locus-tag="An18g01450"
		/number=1
exon	106647..106803	/locus-tag="An18g01450"
		/number=2
gene	<107279..>108340	/locus-tag="An18g01460"
mRNA	join(<107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..>108340)	/locus-tag="An18g01460"
CDS	join(107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..108340)	/locus-tag="An18g01460"

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 Catalytic activity: cyclohexanol
 dehydrogenases convert
 cyclohexanol + NAD(+) <=>
 cyclohexanone + NADH. Function:
 chnA of A. sp. is an alcohol
 dehydrogenases proposed to
 catalyze the conversion of
 cyclohexanol to cyclohexanone (EC
 1. 1. 1. 245). Phenotype:
 cyclohexanol was detected as the
 major intermediate accumulated in
 the chnA mutant of A. sp. Remark:
 chnA of A. sp. is encoded in the
 gene cluster for cyclohexanol
 oxidation. Similarity: the ORF
 shows similarity to several
 dehydrogenases from different
 species and with various
 specificities. Title: strong
 similarity to cyclohexanol
 dehydrogenase chnA - Acinetobacter
 sp"
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		/inference="protein motif:SignalP:2.0"
mat-peptide	join(107388..107740, 107795..107907, 107966..107988, 108045..108097, 108151..108337)	/locus-tag="An18g01460"
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exon	108151..108340	/locus-tag="An18g01460"
		/number=6
gene	<108826..>111209	/locus-tag="An18g01470"
mRNA	join(<108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960, 111135..>111209)	/locus-tag="An18g01470"
CDS	join(108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960,	/locus-tag="An18g01470"

111135..111209)

/EC-number="1.14.-.-"
/inference="profile:COGS:COG0493"
/note="unnamed protein product;
Remark: aflatoxins are
polyketide-derived secondary
metabolites. Remark: moxY of A.
parasiticus is expressed
concurrently with genes involved
in aflatoxin biosynthesis and it
lies on one end of the cluster of
this genes. Therefore moxY of A.
parasiticus is presumably also
involved in aflatoxin
biosynthesis. Similarity: the ORF
shows similarity to monooxygenases
from several species and with
different functions. Title: strong
similarity to monooxygenase moxY
-Aspergillus parasiticus"
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FFPKQEEILQYIHGVADEFSVALK
LVGHTEWEGADWQDSEQCWEVRLREIPSGRKFT
RCRILISAVGGLTNPKHVMLQGIE
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FIPAIADDAASINQFIRHVRKCAP
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VDITNDPVVAVEEQSITTQSGKRF
PADLIADVLDYGRCLRLGSLSRSTMSTGEVVMG
VRDKNIGTVSAAYKHLRRWPWRNF
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STISLVRVLTVVEEKPSLSLL"
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intron	108945..109019
exon	109020..109023
intron	109024..109088
exon	109089..109305
intron	109306..109376
exon	109377..109778
intron	109779..109840
exon	109841..109905
intron	109906..110159
exon	110160..110181

intron	110182..110243	/number=6
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exon	110244..110293	/number=6
		/locus-tag="An18g01470"
intron	110294..110354	/number=7
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exon	110355..110492	/number=7
		/locus-tag="An18g01470"
intron	110493..110523	/number=8
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exon	110524..110752	/number=8
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intron	110753..110865	/number=9
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 sequence:UniProtKB:AB013443.1"
 /note="unnamed protein product;
 Function: eln2 of C. cinereus
 encodes a novel type of microsomal
 cytochrome P450 enzyme, with is
 involved in mushroom
 morphogenesis. Phenotype: a
 dominant mutation of the
 elongationless2 (eln2) gene of the
 mushroom C. cinereus affects
 pattern formation in the
 development of fruit body
 primordia, causing dumpy primordia
 which culminate in mature fruit
 bodies with short stipes.
 Similarity: the ORF shows
 similarity to several cytochrome
 p450 related proteins from
 different species, which have
 different cellular functions.
 Title: strong similarity to
 cytochrome p450 related protein
 eln2 - Coprinus cinereus"
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 YHPIQDLESQQLMFDLLRSNDFDA
 HFERYSGSLMFALAYGFRLSPKGQELRDMRTIQ
 GNFTYAARVGTWIVDAIPVLNLYLP

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gene	complement(<113565..>114733)	/locus-tag="An18g01490"
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                                DR"
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exon      complement(114210..1147 /locus-tag="An18g01490"
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mRNA      complement(join(<115549 /locus-tag="An18g01500"
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16)
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intron    complement(116017..1160 /locus-tag="An18g01500"
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exon      complement(116080..1164 /locus-tag="An18g01500"
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gene      complement(<117672..>11 /locus-tag="An18g01510"
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mRNA      complement(join(<117672 /locus-tag="An18g01510"
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117885..118021,
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118123..118234))

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/note="unnamed protein product;
Remark: the ORF is questionable
due to its suboptimal intron-exon
structure and short lenght Title:
questionable ORF"
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intron    complement(117783..1178 /locus-tag="An18g01510"
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          /inference="similar to AA
sequence:UniProtKB:ENQUTCH.2"
/note="unnamed protein product;
Function: due to the presence of a
putative 'zinc cluster' motif and
its low (16%) but significant
similarity with the DNA-directed
DNA polymerase of hepatitis B
virus,it was assumed that qutH of
A. nidulans is a DNA-binding
protein, which is possibly
involved in the regulation of
genes essential for the
utilisation of protocatechuic
acid. Function: due to the
similarity of the ORF to
oxidoreductases, it is here
assumed that the ORF is encoding a
protein with oxidoreductase
activity. Similarity: the ORF
shows similarity to several
oxidoreductases from different
species. Title: strong similarity
to quinic-acid utilisation gene
qutH - Aspergillus nidulans"
/citation=[10]
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mat-peptide	119227..120294	<pre> /locus-tag="An18g01520" /product="unnamed" </pre>
exon	119176..120297	<pre> /locus-tag="An18g01520" /number=1 </pre>
gene	complement(<120373..>121787)	<pre> /locus-tag="An18g01530" </pre>
mRNA	complement(join(<120373..120856,120912..121419,121479..121515,121584..>121787))	<pre> /locus-tag="An18g01530" </pre>
CDS	complement(join(120373..120856,120912..121419,121479..121515,121584..121787))	<pre> /locus-tag="An18g01530" </pre>

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/note="unnamed protein product;
Function: pth11 of M. grisea is
involved in host surface
recognition for the initiation of
appressorium formation, which is
important in plant infection.
Phenotype: M. grisea pth11 mutants
are nonpathogenic due to a defect
in appressorium differentiation.
Remark: on the same contig another
ORF shows similarity to pth11 of
M. grisea, see 130cg. Similarity:
the ORF is 85 amino acids shorter
at its N-terminus and 155 amino
acids shorter at the C-terminal
end than pth11 of M. grisea.
Title: strong similarity to
integral membrane protein PTH11 -
Magnaporthe grisea"
/citation=[52]
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ISGGFYGAGKHVWAI SVTKLVTLF"

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sequence:UniProtKB:AB014491.1"
/note="unnamed protein product;
Function: TRI101 of F. sporotrichioides conferred significant increased tolerance to the mycotoxin DAS (trichothecene 4,15-diacetoxyscirpenol), which is harmful for vertebrates. Function: TRI101 of F. sporotrichioides converts isotrichodermol to isotrichodermin and is required for the modification of T-2 toxin, which inhibits protein synthesis in eukaryotes. Phenotype: TRI101 mutants of F. sporotrichioides were altered in their abilities to synthesize T-2 toxin and accumulated isotrichodermol and small amounts of 3,15-didecalonectrin and 3-decalonectrin, trichothecenes.
Title: strong similarity to trichothecene
3-O-acetyltransferase TRI101 - Fusarium sporotrichioides"

		/citation=[48] /citation=[53] /citation=[56] /codon-start=1 /protein-id="CAK47227.1" /db-xref="GI:134084194" /translation="MGSIAPDVPTFTPLELIGPR GYMRYVFTFPLGEDYVLEDVSRAL KAGYNAAAQRLPILACEAIPDPTARQDSVMKLQM LGPNAEEPILVKDLRTQDTLPSYA ELKTQHFPVAAFNADTLCRRDIWPTDLGEHLPIS LVQANFIRGGLILTWCILHMAGDG NSFQTMWRVWAEECRAQGVKITDPVVLPPAIFA DREKVMRSSGRNPGRIEDHPEYVV LPFKPPEGLPPKMLAKNHRAQVFYFSPEALAALK KEASPKNASEPRDVPWISTNDALS ALLWRTVMAVQWPLETLESVNQDQESFFNIALNG RLRTDPPVHPNTLGCFLLEYIGVSM PVHKMLTSAQLANLAVLIRQALHQVSNQHTDDVI SLIEQLDDIRKIFPASLVDLPGFN CILTSWVDFALYNLDWGTLGHHIESVRAPHVGV INGLQVVLPNPREGGMEVLVGVA GCLEKLLNDPLWMKYAVAR"
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mRNA	complement(join(<123984..124060, 124183..125132, 125181..125432, 125485..125732, 125913..>127145))	/locus-tag="An18g01550"
CDS	complement(join(123984..124060,124183..125132, 125181..125432, 125485..125732, 125913..127145))	/locus-tag="An18g01550" /note="unnamed protein product; Title: similarity to hypothetical protein AAM43672.1 - Dictyostelium discoideum" /codon-start=1 /protein-id="CAK47228.1" /db-xref="GI:134084195" /translation="MRPIVADVNDNDGHIELKRG LCAVLETIESSGSFLTQDLGLGLA IPGLNIAGLGNIRLPISADDAKAITQCCDRSPYG KGSETLVDESVRKTWQLDPGQFSL QNPLWQQQMDDVDDAVTGLGLTAQSDEVQAELY KLLIYEEGAFFLPHQDTEKADGMF ATLVVCLPSKHEGGTLVASHRGWKIAWSTASSSE FSFSWAAWYADVIHEVRPVTSGYR VALVYNLIHRPLVGLGISGVQTDKLTLLLESWVS DCSGNGQSDHSAWDHHINGDCPPA LVYVLEHQYTVVELSFDRLKGVQVRFGELOKAC QGLDFDLYLANIEKTRMGGVDGRY GNSYWKAHNALEDVLGGNQKFLSVVDASGSEVGK RLPFHGKLLIQEDFFSNRLPDDEK YQGFTGNEAAKATRVYRATLFSEQPDNALTKRNL VRACQTILKKHSSSEMRAKVMQI AIDVDDVILFCQTLVSLEGTMSSEITQTAKVLA

		KHGLEAIRLALERVFQDKPHGPSL PERVSCISKLFREYRAICQERGRAPSVEMLNWES AIISNYLSCYSNDTEPDGRHLVDV LTPLPQEGLFERIIPFLETKIERTACLGKFFVSV YVYSRRGKFDQDAVDAMLKNLLPK FFRGFRVQYKHTSNSGLEFAANCRPTKHTTSIRI DPKTVVGLIKLGDVMDVDNTALFH ALTEYTLDVQARDMPDVFTDFLLPVANGVCENVI TSGGPSTNSERRFVKHILNKYITG YVLPAPLVPPDWKGRSCILCRCYTICASLDTFIED PAVRTRKVMGNDMEHFDRLDD FFFTKTVVGPVGMQMLRIWKTAMMLVSQLHAWN KRARDAKAQLDQLDKHRSLEILG NTYDSLNMHPNLTLPDDHPAATSTAIQAGHPMSG SVVPNITLYRQIDDEYMSACTDEC TNAST"
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CDS	join(127862..127973, 128149..128238, 128310..128432, 128566..128684, 128777..128854, 128935..129026, 129125..129230)	/locus-tag="An18g01560"
		/note="unnamed protein product; Remark: the ORF is questionable due to its suboptimal intron-exon structure. Title: questionable ORF"

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CDS	join(129407..129556, 129604..129720, 129768..129958, 130008..130130, 130176..130256, 130321..130729, 130866..130916)	/locus-tag="An18g01570"

/note="unnamed protein product;
Function: pth11 of M. grisea pth11
is involved in host surface
recognition for the initiation of
appressorium formation, which is
important in plant infection.
Phenotype: M. grisea pth11 mutants
are nonpathogenic due to a defect
in appressorium differentiation.

Remark: on the same contig another ORF shows strong similarity to pth11 of *M. grisea*, see 160wg. Similarity: the ORF is 92 amino acids shorter at the N-terminal end and 165 amino acid its C-terminus than pth11 of *M. grisea*. Title: similarity to integral membrane protein PTH11 - Magnaporthe grisea"
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intron	130131..130175	/locus-tag="An18g01570" /number=4
exon	130176..130256	/locus-tag="An18g01570" /number=5
intron	130257..130320	/locus-tag="An18g01570" /number=5
exon	130321..130729	/locus-tag="An18g01570" /number=6

intron	130730..130865	/locus-tag="An18g01570" /number=6
exon	130866..130916	/locus-tag="An18g01570" /number=7
gene	complement(<131646..>132375)	/locus-tag="An18g01580"
mRNA	complement(join(<131646..132295, 132363..>132375))	/locus-tag="An18g01580"
CDS	complement(join(131646..132295, 132363..132375))	/locus-tag="An18g01580" /EC-number="4.2.1.1" /inference="profile:COGS:COG0288" /inference="profile:PFAM:PF00484" /inference="similar to AA sequence:UniProtKB:AB040135.1" /note="unnamed protein product; Catalytic activity: pcal of P. purpureum converts H(2)CO(3) <=> CO(2) + H(2)O with the usage of zinc as cofactor. Function: carbonic anhydrases catalyze the reversible hydration of carbon dioxide. Remark: an alternate name for pcal of P. purpureum is gtpcal. Similarity: the ORF shows similarity to several carbonic anhydrases from different species and with various cellular functions. Title: strong similarity to carbonic anhydrase pcal - Porphyridium purpureum" /citation=[32] /citation=[62] /codon-start=1 /protein-id="CAK47231.1" /db-xref="GI:134084198" /translation="MAVTDLHSQQPEKPQDPYTK ALTLNHLWAQKTTLQNPSLFPTLA RAQHPQILWIGCSDSRCPETTLDDLKPGDVVFVHR NIANVVNAADVNC AAVVEYAVLHL KVKHVVVCGHTCCGGVGAVLAAPKGERDGEDGEK SVLDAWLSSLKRVDRYASELEGI HGEYERGVRLVELNVLEGVRVLMAMGVVREAVEK GEVEVHGAVYNVGC GVVRELELEV KL"
exon	complement(131646..132295)	/locus-tag="An18g01580"
intron	complement(132296..132362)	/number=1 /locus-tag="An18g01580"
exon	complement(132363..132375)	/number=1 /locus-tag="An18g01580"
gene	complement(<133082..>135202)	/number=2 /locus-tag="An18g01590"
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CDS	complement(join(133082..133214,133277..134939,135000..135045,135113..135202))	/locus-tag="An18g01590" /EC-number="2.3.1.7" /inference="profile:PFAM:PF00755" /inference="similar to AA sequence:PIR:S68958" /note="unnamed protein product; Catalytic activity: cat2 of C. tropicalis catalyses acetyl-CoA + carnitine <=> CoA + O-acetylcarnitine. Function: cat2 of C. tropicalis is specific for the acetylation of short chain fatty acids and may also be involved in the transport of acety-CoA into mitochondria. Similarity: the ORF overlaps with A. niger EST EMBLEST:BE760390. Title: strong similarity to carnitine O-acetyltransferase cat2 - Candida tropicalis inner membrane" /codon-start=1 /protein-id="CAK47232.1" /db-xref="GI:134084199" /translation="MFAASSRNRLSTLPRTLSP ANLLARS AVTPIMAPRRKASSVP EGYKEDLSKGNMLRFEDSLPRLPVPSLEETGRRY LKSVHALVSEAEYERTKKAVEAFV RPGGEGEPLQERLLARAADPKIKNWLLEWWNHAA YLGYRDPVIPYVSFYFYSYRDDRAR RDPAKRAASVATAALEFKRQVDDGSLEPEYMRGQ PMAMSTYQYMFNCCRIPGDSVDYP QKFPAQDNEHIVVVRKNQFFKVPLTVNGKRLNNS ELQRQFERIYEVAQPAPAVGVLTV ANRDLWADARKKLLAAHPANEQALRDISSGFLV CLDNATPVTLEERAHQYWHGDGTN RWFDPKPLQFIINDNGTAGFMGEHSMMDGSPTHRM NDHLNNLIFNHKIDLSEKPVRSDL PDPRPITFHLDPVLEAIDAANKEHRQQISSHEL RVQAYQGYGKGLIKKFKCSPDAYV QMI IQLAYFKMYGKNRPTYESASTRKFQEGRTET IRTVSDSVAFCKAISDPVPREE AVRLRLSALAAHTKYTAEASDGRGVDRHLFGLKK LLREGEKLPALYEDPAFAYSSSWY LSTSQLSSEFFNGYGWSQVIDDGFGIAYMINENS LNFNIVCKRLGAERMSYYLNEAAS DMRDMLMPDLAAQSEKAKM"
exon	complement(133082..133214)	/locus-tag="An18g01590"
intron	complement(133215..133276)	/number=1 /locus-tag="An18g01590"
exon	complement(133277..134939)	/number=1 /locus-tag="An18g01590"
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intron	complement(135046..135112)	/locus-tag="An18g01590"
		/number=3
exon	complement(135113..135202)	/locus-tag="An18g01590"
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mRNA	complement(join(<135940..136119, 136175..136476, 136534..136864, 136972..>137166))	/locus-tag="An18g01600"
CDS	complement(join(135940..136119,136175..136476, 136534..136864, 136972..137166))	/locus-tag="An18g01600"
		/inference="profile:COGS:COG0515"
		/note="unnamed protein product; Function: srpk2 was first found to mediate the interaction and localization of pre-mRNA splicing factors by phosphorylating the SR (serine/arginine-rich) family of splicing factors and therefore probably controls the activity of splicing. Phenotype: overexpression of srpk2 in M. musculus causes disassembly of cotransfected SF2/ASF and endogenous SC35. Similarity: the ORF shows similarity to several protein kinases from different species and with various specificity. Title: strong similarity to serine/arginine-rich protein-specific kinase srpk2 - Mus musculus deleted EC-number 2.7.1.37"
		/citation=[41]
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exon	complement(135940..136119)	/locus-tag="An18g01600"
		/number=1
intron	complement(136120..136119)	/locus-tag="An18g01600"

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74)
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76)      /locus-tag="An18g01600"
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exon      complement(136534..1368 /number=2
64)      /locus-tag="An18g01600"
intron    complement(136865..1369 /number=3
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exon      complement(136972..1371 /number=3
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mRNA      complement(join(<138020 /locus-tag="An18g01610"
..139287,
139338..139723,
139790..>140061))
CDS       complement(join(138020. /locus-tag="An18g01610"
.139287,139338..139723,
139790..140061))

/inference="similar to AA
sequence:PIR:A40711"
/note="unnamed protein product;
Function: srb4 of S. cerevisiae is
a component of the multi
subunitcomplex, which binds to RNA
polymerase II and is essential for
efficient establishment of the
transcription initiation
apparatus. Phenotype: the S.
cerevisiae srb4 the null mutant is
inviabile and srb4 mutants display
global defects in mRNA synthesis.
Remark: an alternate name for srb4
of S. cerevisiae is YER022w.
Title: strong similarity to RNA
polymerase II suppressor protein
Srb4 - Saccharomyces cerevisiae
nucleus"
/citation=[22]
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LYKRRAEILQFAMQAHMEALFALD
FVSLLLSKHTPRQAETSMSAFLKQVAPLGSLNAE
IVEPPPKSEAAVQDVKTVSRGWRA
QNFNAAANKLLNSATRLEEEVASETKYWDEVLA
VKEKGWKVCRLPRERTALGVQYGFL
EATPIFRDRGLAALRRADNGSLILDKGLAPQKTR
TVRVRVKHRGQLTGCSKMPDPIPD
AASVERRILQARDTVYEEELFHELMREARIMGSH
GVTTRQNLVRLPISEDQEILLDLV
DADRETPDEDKIESTEHDVLANGLSHSIRILLAY

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		/number=3
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CDS	complement(join(141613..142684, 142735..143279))	/locus-tag="An18g01620"
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		IKELDRATSPKKKSAPTRLIKHGDKGPECLYSKHL QIGPKYRMELIKLMLENERILGEK AIQDAFDEAFFKTNFWTLWATTFALQPWHSLEVEF RRCLCKHLAEIERLNDVKALDRTK YTIYESVIMPIESYLKSQGVDFHFNAKVNTNLQIN PKEAQTTVSGII IKDNGEQKTIEV RPEDLVMVTLGSTTSATERGSNDKAPAAPPQHSHK EFLDDDWALWIDLMQASTDYGNPF NFHNNVDQSTLESFTVTLRDSDFMERYEKLTTNNK PGTGALLSFSDSNWGLSISVPRQP VCSDQPSSVDVFWGYGLHPEKTGNFVHKPMCHCS GKEILTEVLSQLGMPVDDMLANSI TNPVLMPMATAPLMRRHDYRPEVIPPPQSRNLAL VGQYVEIQDDTTLSMEYSVRGAQM AVFSAMKLNKHPKIERHLLLSVFDLLGGA"
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exon	complement(142735..143279)	/locus-tag="An18g01620"
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mRNA	join(<144032..144169, 144230..145373, 145427..>145578)	/locus-tag="An18g01630"
CDS	join(144032..144169, 144230..145373, 145427..145578)	/locus-tag="An18g01630"
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		IADQLLSVKMVLADGSIVEASDEDNQDLFWAVRG AGQAFGVATEFVFRAHKVRDRFFG GLVYYDVKLPMLVSFANEFDKRQDPKSGFFFGF AAPREIGHMVVLAVLFYDGSAYDG EAFEPILNPNPLINRAAMKSYIEMNSIANVDPV PEGRKSIGGANIMPPLETSLLQNL YSQFKEAMNTYPRMEDSALVFELLPYTKAVQVPI KETACANRGPYYNVGLILCWHDS LDAKMHALQRSIIISKILEAQRDITDDHAVVYPNL AGHDVSAEKLFGANLPRQLKLKKK YDPHNVFRKWHDLAPARSHVEQTDKP"
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intron	144170..144229	/locus-tag="An18g01630" /number=1
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intron	145374..145426	/locus-tag="An18g01630" /number=2
exon	145427..145578	/locus-tag="An18g01630" /number=3
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mRNA	join(<146433..146489, 146546..146952, 146998..147273, 147331..147795, 147845..147954, 148006..>148685)	/locus-tag="An18g01640"
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/EC-number="2.4.1.-"
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 /inference="similar to AA
 sequence:PIR:T00130"
 /note="unnamed protein product;
 Function: TSase of G. frondosa
 catalyzes the trehalose synthesis
 from alpha-D-glucose 1-phosphate
 and D-glucose. Similarity: the ORF
 shows similarity to a
 clock-controlled gene (ccgs) of N.
 crassa with unknown function.
 Title: strong similarity to
 trehalose synthase TSase - Grifola
 frondosa"
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 /citation=[49]
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 TDLVDFLVCTWHALRPNVSDYATDTIIAELKDYR
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 SRLWSELDIVPLVLEHKDRERRHDDQGELATFAG
 WNKKELDERADSMVRKCIRSFSGIG
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 PATWSMAQCFAQDLREREVKVAFF"

		SMTCCGKPDVPTRHLSRFTKSLGVRIKWVFPKP RPGMIPLIRKMQDTLEGQGDPLSD ITINDELLILDFAYANARRYWLCENGPLRPRAEG GVDVVIIDSAPLLTLAILSKQQDP ERPVIFESSLQPQGVSLSGTSSPQSRWDFIRTR LTHVDLVVSLLPKELAPRIMPEEN VGYMSFSVDQLDGQNKPLTDWDVGFYGREFSSLC RTLQMSIIRYPEEQYILHLSQFRP GDGTLCLLHSYQKFCDAYTKEHPGRQVPKLLICH RGPFRTPESTVFYDAAMSQIDSSE TLSTSVCIIPIGAVDQMWNALLTNARALVQLSTL HGVPEMLLAAIQKGPVIAVREAE LFPFVHESENAILVDKGDEEGIARCFSRIFSVD VRQGECDAGFRKLSDSNTTVGNAV CWLYLASKMSRGDKFEPRGADIYKLAREEAGYNE CDWHAV"
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		/locus-tag="An18e01650"
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		/product="tRNA-Lys"
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		/note="codon recognized: AAG"
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CDS	join(149921..149936, 150144..150502, 150577..150603)	/locus-tag="An18g01660"
		/note="unnamed protein product; Remark: the ORF is questionable due to its suboptimal intron-exon structure. Similarity: the ORF overlaps with the 5' region of the A. niger pfkA gene. Title: questionable ORF"
		/codon-start=1

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		/locus-tag="An18g01670"
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		/inference="profile:PFAM:PF00365"
		/inference="similar to AA sequence:SWISSPROT:K6PF.ASPNG"
		/note="Catalytic activity: pfkA of A. niger is catalysing ATP + D-fructose 6-phosphate <=> ADP + D-fructose 1,6-bisphosphate. Function: pfkA of A. niger is active in a key control step of glycolysis. Gene-ID: pfkA Similarity: the ORF overlaps with the sequence of entry EMBL:ANPFKA (A. niger pfkA gene) cytoplasm"
		/citation=[1]
		/citation=[5]
		/citation=[21]
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		/db-xref="InterPro:IPR009161"
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		GKRRITIVIVAEGAQDRHLNKISSS KIKDILTERLNLDTTRVTVLGHTQRGGAACAYDRW LSTLQGVEAVRAVLDMKPEAPSPV ITIRENKILRMPLMDAVQHTKTVTKHIQNKEFAE AMALRDSEFKKEYHFSYINTSTPDH PKLLLLPENKMRIGIIHVGAPAGGMNQATRAAVA YCLTRGHTPLAIHNGFPGLCRHYD DTPICSVREVAWQESDAWVNEGGS DIGTNRGLPG DDLATTAKSFKKFGFDALFVVGGF EAFTAVSQLRQAREKYPEFKIPMTVLPATISNNV PGTEYSLGSDTCLNTLIDFCDAIR QSASSRRRVFVIETQGGKSGYIATTAGLSVGAV AVYIPEEGIDIKMLARDIDFLRDN FARDKGANRAGKII LRNECASSTYTTQVVADMIK EEAKGRFESRAAVPGHFQQGGKPS PMDRIRALRMATKMLHLESYAGKSAD EIAADEL SASVIGIKGSQVLFSPMGGGETGLE ATETDWARRRPKTEFWLELQDTVNILSGRASVNN ATWSCYENA"
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intron	151890..151936	/gene="pfkA" /locus-tag="An18g01670" /number=2
exon	151937..153085	/gene="pfkA" /locus-tag="An18g01670" /number=3
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 /inference="similar to AA
 sequence:UniProtKB:AF281147.1"
 /note="unnamed protein product;
 Catalytic activity: NADH
 dehydrogenases catalyse NADH +
 acceptor <=> NAD(+) + reduced
 acceptor. Function: ndh of P.
 fluorescens is involved in
 colonization of this bacterium.
 Phenotype: in an oxygen-poor
 medium mutant PCL1201 of P.
 fluorescens, which carries a
 mutation in the ndh gene showed a
 decreased growth rate. Remark: the
 sequence of the database entry
 EMBL:ANPFKA (A. niger pfkA gene)
 overlaps with the ORF due a

probably wrong number of 4658 bp
for the coding sequence of the A.
niger protein, which is encoded
3'. Similarity: the ORF is 112
amino acids shorter at its
C-terminal end than ndh of P.
fluorescens. Title: similarity to
NADH dehydrogenase II ndh
-Pseudomonas fluorescens
localisation:mitochondrion"
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LLQVEESTTNNTNKALREIKYDYLVIASGSTPSA
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YPFKLSPTSTSTITETIQSAQHTISTSKKITIIG
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Function: CaMDR1 of C. albicans
the confers insensitivity to the
anti-mitotic drug, benomyl, and to
the dihydrofolate reductase
inhibitor, methotrexate. Remark:

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seven different mutant alleles of CaMDR1 from *C. albicans* showed distinct drug resistance profiles. Similarity: the ORF shows similarity to several major facilitator proteins from different species. Title: strong similarity to benomyl/methotrexate resistance protein MDR1 - *Candida albicans* plasma membrane"

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Remark: the ORF is N-terminally truncated due to contig border.
Title: strong similarity to hypothetical protein encoded by An12g00980 - *Aspergillus niger* [truncated ORF]"

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LOCUS (LOC): AM270325 GenBank (R)
GenBank ACC. NO. (GBN): AM270325
GenBank VERSION (VER): AM270325.1 GI:134081809
CAS REGISTRY NO. (RN): 928583-76-0
SEQUENCE LENGTH (SQL): 226503
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Plants, fungi, algae
DATE (DATE): 24 Mar 2007
DEFINITION (DEF): Aspergillus niger contig An14c0180, complete genome.
SOURCE: Aspergillus niger
ORGANISM (ORGN): Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic
Trichocomaceae; Aspergillus
REFERENCE: 1 (bases 23835 to 25756)
AUTHOR (AU): Jones, S.W.; Luk, K.C.
TITLE (TI): Isolation of a chicken thioredoxin cDNA clone.
Thioredoxin mRNA is differentially expressed in normal
and Rous sarcoma virus-transformed chicken embryo
fibroblasts
JOURNAL (SO): J. Biol. Chem., 263 (20), 9607-9611 (1988)
OTHER SOURCE (OS): CA 109:105752
REFERENCE: 2 (bases 16557 to 19301)
AUTHOR (AU): Robinson, J.S.; Klionsky, D.J.; Banta, L.M.; Emr, S.D.
TITLE (TI): Protein sorting in Saccharomyces cerevisiae: isolation
of mutants defective in the delivery and processing of
multiple vacuolar hydrolases
JOURNAL (SO): Mol. Cell. Biol., 8 (11), 4936-4948 (1988)
OTHER SOURCE (OS): CA 110:20954
REFERENCE: 3 (bases 181479 to 182990)
AUTHOR (AU): Jackson, B.J.; Warren, C.D.; Bugge, B.; Robbins, P.W.
TITLE (TI): Synthesis of lipid-linked oligosaccharides in
Saccharomyces cerevisiae: Man2GlcNAc2 and Man1GlcNAc2
are transferred from dolichol to protein in vivo
JOURNAL (SO): Arch. Biochem. Biophys., 272 (1), 203-209 (1989)
OTHER SOURCE (OS): CA 111:74550
REFERENCE: 4 (bases 197258 to 198879)
AUTHOR (AU): Szumanski, M.B.; Boyle, S.M.
TITLE (TI): Analysis and sequence of the speB gene encoding

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agmatine ureohydrolase, a putrescine biosynthetic enzyme in *Escherichia coli*
JOURNAL (SO): J. Bacteriol., 172 (2), 538-547 (1990)
OTHER SOURCE (OS): CA 113:18542
REFERENCE: 5 (bases 8900 to 10226)
AUTHOR (AU): Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.
TITLE (TI): cDNA sequence for human erythrocyte ankyrin
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 87 (5), 1730-1734 (1990)
OTHER SOURCE (OS): CA 113:146283
REFERENCE: 6 (bases 149275 to 150765)
AUTHOR (AU): Chen, W.N.; Balzi, E.; Capieaux, E.; Choder, M.; Goffeau, A.
TITLE (TI): The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1 and ATE1 loci on chromosome VII from *Saccharomyces cerevisiae* reveals the PDR6 gene, a new member of the genetic network controlling pleiotropic drug resistance
JOURNAL (SO): Yeast, 7 (3), 287-299 (1991)
OTHER SOURCE (OS): CA 116:16482
REFERENCE: 7 (bases 20272 to 22263)
AUTHOR (AU): Tobias, J.W.; Varshavsky, A.
TITLE (TI): Cloning and functional analysis of the ubiquitin-specific protease gene UBP1 of *Saccharomyces cerevisiae*
JOURNAL (SO): J. Biol. Chem., 266 (18), 12021-12028 (1991)
OTHER SOURCE (OS): CA 116:122304
REFERENCE: 8 (bases 92137 to 93393)
AUTHOR (AU): Gosalbes, M.J.; Perez-Gonzalez, J.A.; Gonzalez, R.; Navarro, A.
TITLE (TI): Two beta-glycanase genes are clustered in *Bacillus polymyxa*: molecular cloning, expression, and sequence analysis of genes encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase
JOURNAL (SO): J. Bacteriol., 173 (23), 7705-7710 (1991)
OTHER SOURCE (OS): CA 118:33731
REFERENCE: 9 (bases 159715 to 163074)
AUTHOR (AU): Kumar, V.; Ramakrishnan, S.; Teeri, T.T.; Knowles, J.K.; Hartley, B.S.
TITLE (TI): *Saccharomyces cerevisiae* cells secreting an *Aspergillus niger* beta-galactosidase grow on whey permeate
JOURNAL (SO): Biotechnology (N.Y.), 10 (1), 82-85 (1992)
REFERENCE: 10 (bases 197258 to 198879)
AUTHOR (AU): Szumanski, M.B.; Boyle, S.M.
TITLE (TI): Influence of cyclic AMP, agmatine, and a novel protein encoded by a flanking gene on speB (agmatine ureohydrolase) in *Escherichia coli*
JOURNAL (SO): J. Bacteriol., 174 (3), 758-764 (1992)
OTHER SOURCE (OS): CA 119:21634
REFERENCE: 11 (bases 16557 to 19301)
AUTHOR (AU): Wada, Y.; Ohsumi, Y.; Anraku, Y.
TITLE (TI): Genes for directing vacuolar morphogenesis in *Saccharomyces cerevisiae*. I. Isolation and characterization of two classes of vam mutants
JOURNAL (SO): J. Biol. Chem., 267 (26), 18665-18670 (1992)
OTHER SOURCE (OS): CA 117:105596
REFERENCE: 12 (bases 20272 to 22263)
AUTHOR (AU): Baker, R.T.; Tobias, J.W.; Varshavsky, A.
TITLE (TI): Ubiquitin-specific proteases of *Saccharomyces cerevisiae*. Cloning of UBP2 and UBP3, and functional analysis of the UBP gene family
JOURNAL (SO): J. Biol. Chem., 267 (32), 23364-23375 (1992)
OTHER SOURCE (OS): CA 119:23561

REFERENCE: 13 (bases 16557 to 19301)
AUTHOR (AU): Horazdovsky, B.F.; Emr, S.D.
TITLE (TI): The VPS16 gene product associates with a
sedimentable protein complex and is essential for
vacuolar protein sorting in yeast
JOURNAL (SO): J. Biol. Chem., 268 (7), 4953-4962 (1993)
OTHER SOURCE (OS): CA 118:229898

REFERENCE: 14 (bases 32776 to 34762)
AUTHOR (AU): Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Bogaert, T.;
Van de Ven, W.J.
TITLE (TI): Generation of structural and functional diversity in
furin-like proteins in *Drosophila melanogaster* by
alternative splicing of the *Dfurl* gene
JOURNAL (SO): EMBO J., 12 (5), 1853-1870 (1993)
OTHER SOURCE (OS): CA 120:70454

REFERENCE: 15 (bases 181479 to 182990)
AUTHOR (AU): Jackson, B.J.; Kukuruzinska, M.A.; Robbins, P.
TITLE (TI): Biosynthesis of asparagine-linked oligosaccharides in
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JOURNAL (SO): Glycobiology, 3 (4), 357-364 (1993)
OTHER SOURCE (OS): CA 120:126513

REFERENCE: 16 (bases 22652 to 23365)
AUTHOR (AU): Errabolu, R.; Sanders, M.A.; Salisbury, J.L.
TITLE (TI): Cloning of a cDNA encoding human centrin, an EF-hand
protein of centrosomes and mitotic spindle poles
JOURNAL (SO): J. Cell. Sci., 107 (PT 1), 9-16 (1994)
OTHER SOURCE (OS): CA 122:3785

REFERENCE: 17 (bases 72683 to 73072)
AUTHOR (AU): Ishikawa, A.; Ohta, S.; Matsuoka, K.; Hattori, T.;
Nakamura, K.
TITLE (TI): A family of potato genes that encode Kunitz-type
proteinase inhibitors: structural comparisons and
differential expression
JOURNAL (SO): Plant Cell Physiol., 35 (2), 303-312 (1994)
OTHER SOURCE (OS): CA 121:100855

REFERENCE: 18 (bases 149275 to 150765)
AUTHOR (AU): Lai, M.H.; Bard, M.; Pierson, C.A.; Alexander, J.F.;
Goebel, M.; Carter, G.T.; Kirsch, D.R.
TITLE (TI): The identification of a gene family in the
Saccharomyces cerevisiae ergosterol biosynthesis
pathway
JOURNAL (SO): Gene, 140 (1), 41-49 (1994)
OTHER SOURCE (OS): CA 121:127004

REFERENCE: 19 (bases 176803 to 178484)
AUTHOR (AU): Kil, K.S.; Cunningham, M.W.; Barnett, L.A.
TITLE (TI): Cloning and sequence analysis of a gene encoding a
67-kilodalton myosin-cross-reactive antigen of
Streptococcus pyogenes reveals its similarity with
class II major histocompatibility antigens
JOURNAL (SO): Infect. Immun., 62 (6), 2440-2449 (1994)
OTHER SOURCE (OS): CA 122:73390

REFERENCE: 20 (bases 48251 to 50618)
AUTHOR (AU): Sato, S.; Suzuki, H.; Widyastuti, U.; Hotta, Y.; Tabata, S.
TITLE (TI): Identification and characterization of genes induced
during sexual differentiation in *Schizosaccharomyces*

JOURNAL (SO): Curr. Genet., 26 (1), 31-37 (1994)
OTHER SOURCE (OS): CA 121:197248

REFERENCE: 21 (bases 157327 to 158616)
AUTHOR (AU): Marcus, G.A.; Silverman, N.; Berger, S.L.; Horiuchi, J.;
Guarente, L.
TITLE (TI): Functional similarity and physical association between

JOURNAL (SO): GCN5 and ADA2: putative transcriptional adaptors
 EMBO J., 13 (20), 4807-4815 (1994)
 OTHER SOURCE (OS): CA 122:2700
 REFERENCE: 22 (bases 149275 to 150765)
 AUTHOR (AU): Lees,N.D.; Skaggs,B.; Kirsch,D.R.; Bard,M.
 TITLE (TI): Cloning of the late genes in the ergosterol
 biosynthetic pathway of *Saccharomyces cerevisiae*--a
 review

JOURNAL (SO): Lipids, 30 (3), 221-226 (1995)
 OTHER SOURCE (OS): CA 123:79105
 REFERENCE: 23 (bases 157327 to 158616)
 AUTHOR (AU): Horiuchi,J.; Silverman,N.; Marcus,G.A.; Guarente,L.
 TITLE (TI): ADA3, a putative transcriptional adaptor, consists of
 two separable domains and interacts with ADA2 and GCN5
 in a trimeric complex

JOURNAL (SO): Mol. Cell. Biol., 15 (3), 1203-1209 (1995)
 OTHER SOURCE (OS): CA 122:232629
 REFERENCE: 24 (bases 41237 to 43709)
 AUTHOR (AU): Harris,C.L.; Kolanko,C.J.
 TITLE (TI): Aminoacyl-tRNA synthetase complex in *Saccharomyces*
cerevisiae

JOURNAL (SO): Biochem. J., 309 (PT 1), 321-324 (1995)
 OTHER SOURCE (OS): CA 123:106013
 REFERENCE: 25 (bases 190148 to 191691)
 AUTHOR (AU): Russo,M.W.; Sevetson,B.R.; Milbrandt,J.
 TITLE (TI): Identification of NAB1, a repressor of NGFI-A- and
 Krox20-mediated transcription

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 92 (15), 6873-6877
 (1995)
 OTHER SOURCE (OS): CA 123:277433
 REFERENCE: 26 (bases 163244 to 165037)
 AUTHOR (AU): Saupe,S.; Turcq,B.; Begueret,J.
 TITLE (TI): A gene responsible for vegetative incompatibility in
 the fungus *Podospira anserina* encodes a protein with a
 GTP-binding motif and G beta homologous domain

JOURNAL (SO): Gene, 162 (1), 135-139 (1995)
 OTHER SOURCE (OS): CA 123:331620
 REFERENCE: 27 (bases 20272 to 22263)
 AUTHOR (AU): Hochstrasser,M.
 TITLE (TI): Ubiquitin-dependent protein degradation

JOURNAL (SO): Annu. Rev. Genet., 30, 405-439 (1996)
 OTHER SOURCE (OS): CA 126:43976
 REFERENCE: 28 (bases 65395 to 67116)
 AUTHOR (AU): Stearman,R.; Yuan,D.S.; Yamaguchi-Iwai,Y.;
 Klausner,R.D.; Dancis,A.
 TITLE (TI): A permease-oxidase complex involved in high-affinity
 iron uptake in yeast

JOURNAL (SO): Science, 271 (5255), 1552-1557 (1996)
 OTHER SOURCE (OS): CA 124:225984
 REFERENCE: 29 (bases 157327 to 158616)
 AUTHOR (AU): Wolffe,A.P.; Pruss,D.
 TITLE (TI): Targeting chromatin disruption: Transcription
 regulators that acetylate histones

JOURNAL (SO): Cell, 84 (6), 817-819 (1996)
 OTHER SOURCE (OS): CA 124:251873
 REFERENCE: 30 (bases 190148 to 191691)
 AUTHOR (AU): Svaren,J.; Sevetson,B.R.; Apel,E.D.; Zimonjic,D.B.;
 Milbrandt,J.
 TITLE (TI): NAB2, a corepressor of NGFI-A (Egr-1) and Krox20, is
 induced by proliferative and differentiative stimuli

JOURNAL (SO): Mol. Cell. Biol., 16 (7), 3545-3553 (1996)
 OTHER SOURCE (OS): CA 125:106429

REFERENCE: 31 (bases 157327 to 158616)
AUTHOR (AU): Kuo,M.H.; Brownell,J.E.; Sobel,R.E.; Ranalli,T.A.;
Cook,R.G.; Edmondson,D.G.; Roth,S.Y.; Allis,C.D.
TITLE (TI): Transcription-linked acetylation by Gcn5p of histones
H3 and H4 at specific lysines
JOURNAL (SO): Nature, 383 (6597), 269-272 (1996)
OTHER SOURCE (OS): CA 125:268960

REFERENCE: 32 (bases 137703 to 138530)
AUTHOR (AU): Bang,D.D.; Ketting,R.; de Ruijter,M.; Brandsma,J.A.;
Verhage,R.A.; van de Putte,P.; Brouwer,J.
TITLE (TI): Cloning of Schizosaccharomyces pombe rph16+, a gene
homologous to the Saccharomyces cerevisiae RAD16 gene
JOURNAL (SO): Mutat. Res., 364 (2), 57-71 (1996)
OTHER SOURCE (OS): CA 125:294310

REFERENCE: 33 (bases 2852 to 4742)
AUTHOR (AU): Murone,M.; Simanis,V.
TITLE (TI): The fission yeast dmal gene is a component of the
spindle assembly checkpoint, required to prevent septum
formation and premature exit from mitosis if spindle
function is compromised
JOURNAL (SO): EMBO J., 15 (23), 6605-6616 (1996)
OTHER SOURCE (OS): CA 126:208115

REFERENCE: 34 (bases 157327 to 158616)
AUTHOR (AU): Chiang,Y.C.; Komarnitsky,P.; Chase,D.; Denis,C.L.
TITLE (TI): ADR1 activation domains contact the histone
acetyltransferase GCN5 and the core transcriptional
factor TFIIB
JOURNAL (SO): J. Biol. Chem., 271 (50), 32359-32365 (1996)
OTHER SOURCE (OS): CA 126:128325

REFERENCE: 35 (bases 98558 to 100377)
AUTHOR (AU): Stuke,J.; Carman,G.M.
TITLE (TI): Identification of a novel phosphatase sequence motif
JOURNAL (SO): Protein Sci., 6 (2), 469-472 (1997)
OTHER SOURCE (OS): CA 126:289905

REFERENCE: 36 (bases 51277 to 53277)
AUTHOR (AU): Portman,D.S.; O'Connor,J.P.; Dreyfuss,G.
TITLE (TI): YRA1, an essential Saccharomyces cerevisiae gene,
encodes a novel nuclear protein with RNA annealing
activity
JOURNAL (SO): RNA, 3 (5), 527-537 (1997)
OTHER SOURCE (OS): CA 127:13954

REFERENCE: 37 (bases 65395 to 67116)
AUTHOR (AU): de Silva,D.; Davis-Kaplan,S.; Fergestad,J.; Kaplan,J.
TITLE (TI): Purification and characterization of Fet3 protein, a
yeast homologue of ceruloplasmin
JOURNAL (SO): J. Biol. Chem., 272 (22), 14208-14213 (1997)
OTHER SOURCE (OS): CA 127:77719

REFERENCE: 38 (bases 98558 to 100377)
AUTHOR (AU): Qie,L.; Nagiec,M.M.; Baltisberger,J.A.; Lester,R.L.;
Dickson,R.C.
TITLE (TI): Identification of a Saccharomyces gene, LCB3, necessary
for incorporation of exogenous long chain bases into
sphingolipids
JOURNAL (SO): J. Biol. Chem., 272 (26), 16110-16117 (1997)
OTHER SOURCE (OS): CA 127:146248

REFERENCE: 39 (bases 19354 to 19996)
AUTHOR (AU): Lussier,M.; White,A.M.; Sheraton,J.; di Paolo,T.;
Treadwell,J.; Southard,S.B.; Horenstein,C.I.;
Chen-Weiner,J.; Ram,A.F.; Kapteyn,J.C.; Roemer,T.W.;
Vo,D.H.; Bondoc,D.C.; Hall,J.; Zhong,W.W.; Sdicu,A.M.;
Davies,J.; Klis,F.M.; Robbins,P.W.; Bussey,H.
TITLE (TI): Large scale identification of genes involved in cell

surface biosynthesis and architecture in *Saccharomyces cerevisiae*

JOURNAL (SO): Genetics, 147 (2), 435-450 (1997)
 OTHER SOURCE (OS): CA 127:327291
 REFERENCE: 40 (bases 65395 to 67116)
 AUTHOR (AU): Yuan,D.S.; Dancis,A.; Klausner,R.D.
 TITLE (TI): Restriction of copper export in *Saccharomyces cerevisiae* to a late Golgi or post-Golgi compartment in the secretory pathway

JOURNAL (SO): J. Biol. Chem., 272 (41), 25787-25793 (1997)
 OTHER SOURCE (OS): CA 127:343694
 REFERENCE: 41 (bases 183872 to 189440)
 AUTHOR (AU): Wood,K.W.; Sakowicz,R.; Goldstein,L.S.; Cleveland,D.W.
 TITLE (TI): CENP-E is a plus end-directed kinetochore motor required for metaphase chromosome alignment

JOURNAL (SO): Cell, 91 (3), 357-366 (1997)
 OTHER SOURCE (OS): CA 128:45048
 REFERENCE: 42 (bases 16557 to 19301)
 AUTHOR (AU): Rieder,S.E.; Emr,S.D.
 TITLE (TI): A novel RING finger protein complex essential for a late step in protein transport to the yeast vacuole

JOURNAL (SO): Mol. Biol. Cell, 8 (11), 2307-2327 (1997)
 OTHER SOURCE (OS): CA 128:32213
 REFERENCE: 43 (bases 218542 to 219708)
 AUTHOR (AU): Nakamura,T.; Ohmoto,T.; Hirata,D.; Tsuchiya,E.; Miyakawa,T.
 TITLE (TI): Yeast Crv4/Ttp1, a predicted type II membrane protein, is involved in an event important for growth, functionally overlapping with the event regulated by calcineurin- and Mpk1-mediated pathways

JOURNAL (SO): Mol. Gen. Genet., 256 (5), 481-487 (1997)
 OTHER SOURCE (OS): CA 128:138463
 REFERENCE: 44 (bases 163244 to 165037)
 AUTHOR (AU): Espagne,E.; Balhadere,P.; Begueret,J.; Turcq,B.
 TITLE (TI): Reactivity in vegetative incompatibility of the HET-E protein of the fungus *Podospora anserina* is dependent on GTP-binding activity and a WD40 repeated domain

JOURNAL (SO): Mol. Gen. Genet., 256 (6), 620-627 (1997)
 OTHER SOURCE (OS): CA 128:214667
 REFERENCE: 45 (bases 98558 to 100377)
 AUTHOR (AU): Mao,C.; Wadleigh,M.; Jenkins,G.M.; Hannun,Y.A.; Obeid,L.M.
 TITLE (TI): Identification and characterization of *Saccharomyces cerevisiae* dihydrosphingosine-1-phosphate phosphatase

JOURNAL (SO): J. Biol. Chem., 272 (45), 28690-28694 (1997)
 OTHER SOURCE (OS): CA 128:72216
 REFERENCE: 46 (bases 103137 to 103945)
 AUTHOR (AU): Kondoh,O.; Tachibana,Y.; Ohya,Y.; Arisawa,M.; Watanabe,T.
 TITLE (TI): Cloning of the RH01 gene from *Candida albicans* and its regulation of beta-1,3-glucan synthesis

JOURNAL (SO): J. Bacteriol., 179 (24), 7734-7741 (1997)
 OTHER SOURCE (OS): CA 128:111391
 REFERENCE: 47 (bases 67552 to 68735)
 AUTHOR (AU): Gonzalez,F.J.; Montes,J.; Martin,F.; Lopez,M.C.; Ferminan,E.; Catalan,J.; Galan,M.A.; Dominguez,A.
 TITLE (TI): Molecular cloning of TvDAO1, a gene encoding a D-amino acid oxidase from *Trigonopsis variabilis* and its expression in *Saccharomyces cerevisiae* and *Kluyveromyces lactis*

JOURNAL (SO): Yeast, 13 (15), 1399-1408 (1997)
 OTHER SOURCE (OS): CA 128:150109

REFERENCE: 48 (bases 41237 to 43709)
AUTHOR (AU): Motorin, Y.; Le Caer, J.P.; Waller, J.P.
TITLE (TI): Cysteinyl-tRNA synthetase from *Saccharomyces cerevisiae*. Purification, characterization and assignment to the genomic sequence YNL247w
JOURNAL (SO): *Biochimie*, 79 (12), 731-740 (1997)
OTHER SOURCE (OS): CA 129:24853

REFERENCE: 49 (bases 98558 to 100377)
AUTHOR (AU): Mandala, S.M.; Thornton, R.; Tu, Z.; Kurtz, M.B.; Nickels, J.; Broach, J.; Menzeleev, R.; Spiegel, S.
TITLE (TI): Sphingoid base 1-phosphate phosphatase: a key regulator of sphingolipid metabolism and stress response
JOURNAL (SO): *Proc. Natl. Acad. Sci. U.S.A.*, 95 (1), 150-155 (1998)
OTHER SOURCE (OS): CA 128:151503

REFERENCE: 50 (bases 65395 to 67116)
AUTHOR (AU): Gaxiola, R.A.; Yuan, D.S.; Klausner, R.D.; Fink, G.R.
TITLE (TI): The yeast CLC chloride channel functions in cation homeostasis
JOURNAL (SO): *Proc. Natl. Acad. Sci. U.S.A.*, 95 (7), 4046-4050 (1998)
OTHER SOURCE (OS): CA 128:319139

REFERENCE: 51 (bases 151141 to 153445)
AUTHOR (AU): Cazelle, B.; Pokorska, A.; Hull, E.; Green, P.M.; Stanway, G.; Scazzocchio, C.
TITLE (TI): Sequence, exon-intron organization, transcription and mutational analysis of *prnA*, the gene encoding the transcriptional activator of the *prn* gene cluster in *Aspergillus nidulans*
JOURNAL (SO): *Mol. Microbiol.*, 28 (2), 355-370 (1998)
OTHER SOURCE (OS): CA 129:63816

REFERENCE: 52 (bases 48251 to 50618)
AUTHOR (AU): Lubkowitz, M.A.; Barnes, D.; Breslav, M.; Burchfield, A.; Naider, F.; Becker, J.M.
TITLE (TI): *Schizosaccharomyces pombe* *isp4* encodes a transporter representing a novel family of oligopeptide transporters
JOURNAL (SO): *Mol. Microbiol.*, 28 (4), 729-741 (1998)
OTHER SOURCE (OS): CA 129:119284

REFERENCE: 53 (bases 54264 to 55012)
AUTHOR (AU): Babst, M.; Wendland, B.; Estepa, E.J.; Emr, S.D.
TITLE (TI): The Vps4p AAA ATPase regulates membrane association of a Vps protein complex required for normal endosome function
JOURNAL (SO): *EMBO J.*, 17 (11), 2982-2993 (1998)
OTHER SOURCE (OS): CA 129:146701

REFERENCE: 54 (bases 149275 to 150765)
AUTHOR (AU): Silve, S.; Dupuy, P.H.; Ferrara, P.; Loison, G.
TITLE (TI): Human lamin B receptor exhibits sterol C14-reductase activity in *Saccharomyces cerevisiae*
JOURNAL (SO): *Biochim. Biophys. Acta*, 1392 (2-3), 233-244 (1998)
OTHER SOURCE (OS): CA 129:146116

REFERENCE: 55 (bases 27949 to 28578)
AUTHOR (AU): Caldas, C.; Kim, M.H.; MacGregor, A.; Cain, D.; Aparicio, S.; Wiedemann, L.M.
TITLE (TI): Isolation and characterization of a pufferfish MLL (mixed lineage leukemia)-like gene (*fMll*) reveals evolutionary conservation in vertebrate genes related to *Drosophila trithorax*
JOURNAL (SO): *Oncogene*, 16 (25), 3233-3241 (1998)
OTHER SOURCE (OS): CA 129:171330

REFERENCE: 56 (bases 218542 to 219708)
AUTHOR (AU): Rayner, J.C.; Munro, S.
TITLE (TI): Identification of the MNN2 and MNN5

mannosyltransferases required for forming and extending the mannose branches of the outer chain mannans of *Saccharomyces cerevisiae*
JOURNAL (SO): J. Biol. Chem., 273 (41), 26836-26843 (1998)
OTHER SOURCE (OS): CA 130:22764
REFERENCE: 57 (bases 218542 to 219708)
AUTHOR (AU): Lussier,M.; Sdicu,A.M.; Bussey,H.
TITLE (TI): The KTR and MNN1 mannosyltransferase families of *Saccharomyces cerevisiae*

JOURNAL (SO): Biochim. Biophys. Acta, 1426 (2), 323-334 (1999)
OTHER SOURCE (OS): CA 130:293055
REFERENCE: 58 (bases 154037 to 156562)
AUTHOR (AU): de Vries,R.P.; Visser,J.; de Graaff,L.H.
TITLE (TI): CreA modulates the XlnR-induced expression on xylose of *Aspergillus niger* genes involved in xylan degradation

JOURNAL (SO): Res. Microbiol., 150 (4), 281-285 (1999)
OTHER SOURCE (OS): CA 131:180701
REFERENCE: 59 (bases 80610 to 81592)
AUTHOR (AU): Ui,S.; Mimura,A.; Ohkuma,M.; Kudo,T.
TITLE (TI): Formation of a chiral acetoinic compound from diacetyl by *Escherichia coli* expressing meso-2,3-butanediol dehydrogenase

JOURNAL (SO): Lett. Appl. Microbiol., 28 (6), 457-460 (1999)
OTHER SOURCE (OS): CA 131:225912
REFERENCE: 60 (bases 211445 to 212528)
AUTHOR (AU): Krappmann,S.; Helmstaedt,K.; Gerstberger,T.; Eckert,S.; Hoffmann,B.; Hoppert,M.; Schnappauf,G.; Braus,G.H.
TITLE (TI): The *aroC* gene of *Aspergillus nidulans* codes for a monofunctional, allosterically regulated chorismate mutase

JOURNAL (SO): J. Biol. Chem., 274 (32), 22275-22282 (1999)
OTHER SOURCE (OS): CA 131:268796
REFERENCE: 61 (bases 137703 to 138530)
AUTHOR (AU): Lombaerts,M.; Peltola,P.H.; Visse,R.; den Dulk,H.; Brouwer,J.
TITLE (TI): Characterization of the *rhp7(+)* and *rhp16(+)* genes in *Schizosaccharomyces pombe*

JOURNAL (SO): Nucleic Acids Res., 27 (17), 3410-3416 (1999)
OTHER SOURCE (OS): CA 132:809
REFERENCE: 62
AUTHOR (AU): Tsai,H.F.; Wheeler,M.H.; Chang,Y.C.; Kwon-Chung,K.J.
TITLE (TI): A developmentally regulated gene cluster involved in conidial pigment biosynthesis in *Aspergillus fumigatus*

JOURNAL (SO): J. Bacteriol., 181 (20), 6469-6477 (1999)
OTHER SOURCE (OS): CA 132:45624
REFERENCE: 63
AUTHOR (AU): DeZwaan,T.M.; Carroll,A.M.; Valent,B.; Sweigard,J.A.
TITLE (TI): *Magnaporthe grisea* *pth1lp* is a novel plasma membrane protein that mediates appressorium differentiation in response to inductive substrate cues

JOURNAL (SO): Plant Cell, 11 (10), 2013-2030 (1999)
OTHER SOURCE (OS): CA 132:47358
REFERENCE: 64 (bases 20272 to 22263)
AUTHOR (AU): Layfield,R.; Franklin,K.; Landon,M.; Walker,G.; Wang,P.; Ramage,R.; Brown,A.; Love,S.; Urquhart,K.; Muir,T.; Baker,R.; Mayer,R.J.
TITLE (TI): Chemically synthesized ubiquitin extension proteins detect distinct catalytic capacities of deubiquitinating enzymes

JOURNAL (SO): Anal. Biochem., 274 (1), 40-49 (1999)
OTHER SOURCE (OS): CA 132:20406
REFERENCE: 65 (bases 55690 to 56601)

AUTHOR (AU): Munoz,M.J.; Bejarano,E.R.; Daga,R.R.; Jimenez,J.
TITLE (TI): The identification of Wos2, a p23 homologue that interacts with Wee1 and Cdc2 in the mitotic control of fission yeasts

JOURNAL (SO): Genetics, 153 (4), 1561-1572 (1999)
OTHER SOURCE (OS): CA 132:177833

REFERENCE: 66 (bases 149275 to 150765)
AUTHOR (AU): Zweytick,D.; Hrastnik,C.; Kohlwein,S.D.; Daum,G.
TITLE (TI): Biochemical characterization and subcellular localization of the sterol C-24(28) reductase, erg4p, from the yeast saccharomyces cerevisiae

JOURNAL (SO): FEBS Lett., 470 (1), 83-87 (2000)
OTHER SOURCE (OS): CA 132:331762

REFERENCE: 67 (bases 51277 to 53277)
AUTHOR (AU): Cole,C.N.
TITLE (TI): mRNA export: the long and winding road
JOURNAL (SO): Nat. Cell Biol., 2 (4), E55-E58 (2000)
OTHER SOURCE (OS): CA 133:27711

REFERENCE: 68 (bases 51277 to 53277)
AUTHOR (AU): Stutz,F.; Bachi,A.; Doerks,T.; Braun,I.C.; Seraphin,B.; Wilm,M.; Bork,P.; Izaurrealde,E.
TITLE (TI): REF, an evolutionary conserved family of hnRNP-like proteins, interacts with TAP/Mex67p and participates in mRNA nuclear export

JOURNAL (SO): RNA, 6 (4), 638-650 (2000)
OTHER SOURCE (OS): CA 133:70318

REFERENCE: 69 (bases 163244 to 165037)
AUTHOR (AU): Loubradou,G.; Turcq,B.
TITLE (TI): Vegetative incompatibility in filamentous fungi: a roundabout way of understanding the phenomenon

JOURNAL (SO): Res. Microbiol., 151 (4), 239-245 (2000)
OTHER SOURCE (OS): CA 133:234784

REFERENCE: 70 (bases 166037 to 167516)
AUTHOR (AU): Yu,J.; Woloshuk,C.P.; Bhatnagar,D.; Cleveland,T.E.
TITLE (TI): Cloning and characterization of avfA and omtB genes involved in aflatoxin biosynthesis in three Aspergillus species

JOURNAL (SO): Gene, 248 (1-2), 157-167 (2000)
OTHER SOURCE (OS): CA 133:345391

REFERENCE: 71 (bases 143978 to 145355)
AUTHOR (AU): Sanders,P.M.; Lee,P.Y.; Biesgen,C.; Boone,J.D.; Beals,T.P.; Weiler,E.W.; Goldberg,R.B.
TITLE (TI): The arabidopsis DELAYED DEHISCENCE1 gene encodes an enzyme in the jasmonic acid synthesis pathway

JOURNAL (SO): Plant Cell, 12 (7), 1041-1061 (2000)
OTHER SOURCE (OS): CA 134:25937

REFERENCE: 72 (bases 145510 to 146577)
AUTHOR (AU): Cheng,Q.; Thomas,S.M.; Kostichka,K.; Valentine,J.R.; Nagarajan,V.
TITLE (TI): Genetic analysis of a gene cluster for cyclohexanol oxidation in Acinetobacter sp. Strain SE19 by in vitro transposition

JOURNAL (SO): J. Bacteriol., 182 (17), 4744-4751 (2000)
OTHER SOURCE (OS): CA 134:37832

REFERENCE: 73 (bases 163244 to 165037)
AUTHOR (AU): Saupe,S.J.
TITLE (TI): Molecular genetics of heterokaryon incompatibility in filamentous ascomycetes

JOURNAL (SO): Microbiol. Mol. Biol. Rev., 64 (3), 489-502 (2000)
OTHER SOURCE (OS): CA 134:27321

REFERENCE: 74 (bases 128987 to 130729)
AUTHOR (AU): Tanaka,A.; Tsuge,T.

TITLE (TI): Structural and functional complexity of the genomic region controlling AK-toxin biosynthesis and pathogenicity in the Japanese pear pathotype of *Alternaria alternata*
 JOURNAL (SO): Mol. Plant Microbe Interact., 13 (9), 975-986 (2000)
 OTHER SOURCE (OS): CA 134:96037
 REFERENCE: 75 (bases 143978 to 145355)
 AUTHOR (AU): Stintzi,A.; Browse,J.
 TITLE (TI): The Arabidopsis male-sterile mutant, *opr3*, lacks the 12-oxophytodienoic acid reductase required for jasmonate synthesis
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 97 (19), 10625-10630 (2000)
 OTHER SOURCE (OS): CA 133:293530
 REFERENCE: 76 (bases 54264 to 55012)
 AUTHOR (AU): Amerik,A.Y.; Nowak,J.; Swaminathan,S.; Hochstrasser,M.
 TITLE (TI): The Doa4 deubiquitinating enzyme is functionally linked to the vacuolar protein-sorting and endocytic pathways
 JOURNAL (SO): Mol. Biol. Cell, 11 (10), 3365-3380 (2000)
 OTHER SOURCE (OS): CA 134:82296
 REFERENCE: 77 (bases 208451 to 210658)
 AUTHOR (AU): Tieu,Q.; Nunnari,J.
 TITLE (TI): Mdvlp is a WD repeat protein that interacts with the dynamin-related GTPase, Dnm1p, to trigger mitochondrial division
 JOURNAL (SO): J. Cell Biol., 151 (2), 353-366 (2000)
 OTHER SOURCE (OS): CA 134:52741
 REFERENCE: 78 (bases 208451 to 210658)
 AUTHOR (AU): Mozdy,A.D.; McCaffery,J.M.; Shaw,J.M.
 TITLE (TI): Dnm1p GTPase-mediated mitochondrial fission is a multi-step process requiring the novel integral membrane component Fis1p
 JOURNAL (SO): J. Cell Biol., 151 (2), 367-380 (2000)
 OTHER SOURCE (OS): CA 134:52934
 REFERENCE: 79 (bases 94126 to 97982)
 AUTHOR (AU): Kadoya,T.; Kishida,S.; Fukui,A.; Hinoi,T.; Michiue,T.; Kikuchi,A.
 TITLE (TI): Inhibition of Wnt signaling pathway by a novel axin-binding protein
 JOURNAL (SO): J. Biol. Chem., 275 (47), 37030-37037 (2000)
 OTHER SOURCE (OS): CA 134:233219
 REFERENCE: 80 (bases 80610 to 81592)
 AUTHOR (AU): Ui,S.; Takusagawa,Y.; Ohtsuki,T.; Mimura,A.; Ohkuma,M.; Kudo,T.
 TITLE (TI): Stereochemical applications of the expression of the L-2,3-butanediol dehydrogenase gene in *Escherichia coli*
 JOURNAL (SO): Lett. Appl. Microbiol., 32 (2), 93-98 (2001)
 OTHER SOURCE (OS): CA 135:353434
 REFERENCE: 81 (bases 80610 to 81592)
 AUTHOR (AU): Otagiri,M.; Kurisu,G.; Ui,S.; Takusagawa,Y.; Ohkuma,M.; Kudo,T.; Kusunoki,M.
 TITLE (TI): Crystal structure of meso-2,3-butanediol dehydrogenase in a complex with NAD⁺ and inhibitor mercaptoethanol at 1.7 Å resolution for understanding of chiral substrate recognition mechanisms
 JOURNAL (SO): J. Biochem., 129 (2), 205-208 (2001)
 OTHER SOURCE (OS): CA 135:2180
 REFERENCE: 82 (bases 41237 to 43709)
 AUTHOR (AU): Davidson,E.; Caffarella,J.; Vitseva,O.; Hou,Y.M.; King,M.P.
 TITLE (TI): Isolation of two cDNAs encoding functional human cytoplasmic cysteinyl-tRNA synthetase

JOURNAL (SO): Biol. Chem., 382 (3), 399-406 (2001)
 OTHER SOURCE (OS): CA 135:118589
 REFERENCE: 83 (bases 119272 to 121189)
 AUTHOR (AU): Cukovic,D.; Ehlting,J.; VanZiffle,J.A.; Douglas,C.J.
 TITLE (TI): Structure and evolution of 4-coumarate:coenzyme A
 ligase (4CL) gene families
 JOURNAL (SO): Biol. Chem., 382 (4), 645-654 (2001)
 OTHER SOURCE (OS): CA 136:145906
 REFERENCE: 84 (bases 87776 to 89339)
 AUTHOR (AU): Gassama-Diagne,A.; Hullin-Matsuda,F.; Li,R.Y.;
 Nauze,M.; Ragab,A.; Pons,V.; Delagebeaudeuf,C.;
 Simon,M.F.; Fauvel,J.; Chap,H.
 TITLE (TI): Enterophilins, a new family of leucine zipper proteins
 bearing a b30.2 domain and associated with enterocyte
 differentiation
 JOURNAL (SO): J. Biol. Chem., 276 (21), 18352-18360 (2001)
 OTHER SOURCE (OS): CA 136:114413
 REFERENCE: 85 (bases 80610 to 81592)
 AUTHOR (AU): Otagiri,M.; Kurisu,G.; Swaminathan,S.; Ui,S.;
 Yoneda,S.; Ohkuma,M.; Kudo,T.; Kusunoki,M.
 TITLE (TI): Crystallization and preliminary X-ray studies of
 meso-2,3-butanediol dehydrogenase from Klebsiella
 pneumoniae IAM1063
 JOURNAL (SO): Acta Crystallogr. D Biol. Crystallogr., 57 (PT 6),
 857-859 (2001)
 REFERENCE: 86 (bases 51277 to 53277)
 AUTHOR (AU): Zenklusen,D.; Vinciguerra,P.; Strahm,Y.; Stutz,F.
 TITLE (TI): The yeast hnRNP-Like proteins Yralp and Yra2p
 participate in mRNA export through interaction with
 Mex67p
 JOURNAL (SO): Mol. Cell. Biol., 21 (13), 4219-4232 (2001)
 OTHER SOURCE (OS): CA 135:177841
 REFERENCE: 87 (bases 1 to 226503)
 AUTHOR (AU): Pel,H.J.; de Winde,J.H.; Archer,D.B.; Dyer,P.S.;
 Hofmann,G.; Schaap,P.J.; Turner,G.; de Vries,R.P.;
 Albang,R.; Albermann,K.; Andersen,M.R.; Bendtsen,J.D.;
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 Mortimer,M.A.; Nielsen,J.; Oliver,S.G.; Olsthoorn,M.;
 Pal,K.; van Peij,N.N.; Ram,A.F.; Rinas,U.; Roubos,J.A.;
 Sagt,C.M.; Schmoll,M.; Sun,J.; Ussery,D.; Varga,J.;
 Vervecken,W.; van de Vondervoort,P.J.; Wedler,H.;
 Wosten,H.A.; Zeng,A.P.; van Ooyen,A.J.; Visser,J.;
 Stam,H.
 TITLE (TI): Genome sequencing and analysis of the versatile cell
 factory *Aspergillus niger* CBS 513.88
 JOURNAL (SO): Nat. Biotechnol., 25 (2), 221-231 (2007)
 OTHER SOURCE (OS): CA 146:310276
 REFERENCE: 88 (bases 1 to 226503)
 AUTHOR (AU): Pel,H.J.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O.
 Box 1, 2600 MA Delft, THE NETHERLANDS

FEATURES (FEAT):

Feature Key	Location	Qualifier
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intron	1324..1419	/locus-tag="An14g05040" /number=1
exon	1420..1491	/locus-tag="An14g05040" /number=2
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intron	4086..4148	/locus-tag="An14g05050"
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exon	complement(5604..5620)	/locus-tag="An14g05060"
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gene	complement(<6405..>7365	/locus-tag="An14g05070"
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CDS	complement(join(6405..6	/locus-tag="An14g05070"
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		protein X4G11.070 - Neurospora crassa"
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intron	complement(7161..7214)	/locus-tag="An14g05070"
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exon	complement(7215..7365)	/locus-tag="An14g05070"
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gene	complement(<8900..>10226)	/locus-tag="An14g05080"
mRNA	complement(join(<8900..9282,9368..9550,9634..9898,10206..>10226))	/locus-tag="An14g05080"
CDS	complement(join(8900..9282,9368..9550,9634..9898,10206..10226))	/locus-tag="An14g05080"

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 /note="unnamed protein product;
 Function: many ankyrin repeat
 regions are known to function as
 protein-protein interaction
 domains. Remark: closest manual
 BLASTP homologue:
 SWISSPROT:ANK1-HUMAN. Similarity:
 ankyrin repeats (ANK) are tandemly
 repeated modules of about 33 amino
 acids, that occur in a large
 number of functionally diverse
 proteins mainly from eukaryotes.
 Similarity: the predicted ORF
 shows similarity also to the ZU5
 domain present in ZO-1 and
 Unc5-like netrin receptors, which
 function remains unknown.
 Similarity: the similarity to
 ankyrin of H. sapiens and other
 proteins is mainly due to the
 presence of two ankyrin repeats.
 Title: weak similarity to ankyrin
 (variant 2.1) -Homo sapiens"
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exon	complement(8900..9282)	/locus-tag="An14g05080"
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exon	complement(10206..10226)	/locus-tag="An14g05080"
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		/number=4
gene	<11182..>11344	/locus-tag="An14g05090"
mRNA	join(<11182..11234, 11281..>11344)	/locus-tag="An14g05090"
CDS	join(11182..11234, 11281..11344)	/locus-tag="An14g05090"
		/note="Similarity: BLASTP identifies a stretch of similarity to D. melanogaster genomic fragment CG6456; there is no sufficient reason to consider such a similarity significant." /codon-start=1 /product="hypothetical protein" /protein-id="CAK42070.1" /db-xref="GI:134081815" /translation="MAGSPPNSFPGGNGLSEEF GWLPGGKPTNCNETIGSR"
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intron	11235..11280	/locus-tag="An14g05090"
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gene	<12054..>13438	/locus-tag="An14g05100"
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		Nostoc sp"
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		/note="unnamed protein product;
		Similarity: the predicted ORF
		contains an EF-hand,the most
		common domain responsible for
		calcium binding in proteins like
		calmodulin, myosin regulatory
		light chains,parvalbumins,
		troponins C, and neuronal calcium
		sensors. Title: weak similarity to
		hypothetical protein AT4g01140 -
		Arabidopsis thaliana"
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		SSAAIEKIEGVKALLLSSQEKIYG
		RLSNCSSDAVSPRNVLEKGVKRDDDDDG
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mRNA	complement(join(<14885.. .15101,15159..15313, 15370..15531, 15585..15698, 15751..15900, 15955..16104, 16161..>16307))	/locus-tag="An14g05120"
CDS	complement(join(14885.. 15101,15159..15313, 15370..15531, 15585..15698, 15751..15900, 15955..16104, 16161..16307))	/inference="profile:COGS:COG0714" /inference="similar to AA sequence:UniProtKB:NC17E5.27" /note="unnamed protein product; Function: MoxR is a poorly characterized bacterial protein which may be involved in the regulation of formation of active methanol dehydrogenase. Similarity: the predicted ORF shows weak similarity to many putative proteins classified as MoxR-like ATPases. Title: strong similarity to hypothetical conserved protein 17E5.290 - Neurospora crassa" /codon-start=1 /protein-id="CAK42073.1" /db-xref="GI:134081818" /translation="MEDGSEISRLAPELSDLEVA LFLCLAAHQHCRIDTTDANIHDVA KELALICTNTFGLSYSILDCSSATSLDDFRAELL PPGVYRSSYARPSRSLTTESAGM ISSYHDLRDKHGRKLSAPIEHKQEVVNVVIAKNF NHVNDNIQREALELMHASKQLTTPA GVLEAPNNFLFLPLIVRDETHPINPHLNDYLFIS HFHDTEDGYVYLEENNDWLSDGQL SASSVIHKPEAQMKKGHPYVDSTLLGQLQQQLSTT VSMGADIARYQQDIVVFLRLSRV AGGISTRNLYFKSFSKLLAVLHGIDFLTIPSIVA LAARKVFRHRIIVAKPEEDRSLQY GSDLHAVSQVLEYANPDSILDGVLTLTLEAPL"
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17088..17676,
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19053..19301)

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/inference="profile:PFAM:PF04841"
/note="unnamed protein product;
Complex: VPS16 of S. cerevisiae is
a component of the so called class
C Vps complex, required for
vacuolar protein sorting and
morphology. Function: VPS16 of S.
cerevisiae is required for
vacuolar protein sorting and
vacuolar biogenesis and stability.
Phenotype: S. cerevisiae VPS16
mutants have pleiotropic defects
in vacuolar morphology and
vacuolar protein targeting. Title:
strong similarity to vacuolar
protein sorting-associated protein

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Vps16 - *Saccharomyces cerevisiae*
 vacuole"
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 VITEDGTVRRYFGLHGDFTSFSLGNGAEDYGVRA
 CRFWTSGFVALLSNNQLVAVSNYD
 EPRRLLAPCEGEVSSWSLIPPAYTLRSVEVL
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 EYDPESRVTPRTVDWCGDDAVVIA
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 ASFGKSVLDLYNSDEFVEMTEKLRVLKAVRDYQI
 GLPLSYEQYMRLTPERLIERLVNR
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 DDDAVCKLIVQRLEGKPGISFELI
 AQTAYDEGRAHLATQLLNHEPRAGKQVPLLLDME
 EDEIALDKAIESGDVDLVNYVLLH
 LKTKLPLASFFRTINTRPMASALVETTARGQDTE
 LLKDLFYQDDRPIDGSNVLLSEAL
 DATDLPRKTEKLQLASRLSDSKDPSVVLQKLL
 NEASQLLKVQEALDKDLADRSEFL
 GLSLNETIYRLIRSGYGKRAQKIQSEFRMPEKTF
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 KSPIGWEPFYNEILGAGNTKLASLFVPKCTNLPA
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intron	16865..16909	/locus-tag="An14g05130" /number=2
exon	16910..17038	/locus-tag="An14g05130" /number=3
intron	17039..17087	/locus-tag="An14g05130" /number=3
exon	17088..17676	/locus-tag="An14g05130" /number=4
intron	17677..17725	/locus-tag="An14g05130" /number=4
exon	17726..18996	/locus-tag="An14g05130" /number=5
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exon	19053..19301	/locus-tag="An14g05130" /number=6
gene	complement (<19354..>19996)	/locus-tag="An14g05140"

mRNA	complement(join(<19354..19554,19615..19907,19981..>19996))	/locus-tag="An14g05140"
CDS	complement(join(19354..19554,19615..19907,19981..19996))	/locus-tag="An14g05140"
		/note="unnamed protein product; Phenotype: ECM1 mutation in S. cerevisiae causes perturbation of the cell surface. Remark: ECM1 of S. cerevisiae is also called YAL059w. Title: similarity to Ecml - Saccharomyces cerevisiae" /citation=[39] /codon-start=1 /protein-id="CAK42075.1" /db-xref="GI:134081820" /translation="MAKSRPQSKHSRAARRAASP SLDVDKSLTSLPRAEETTVQRDSI LSERANAGVSKKQSKGKAKTRAQRLRQQKVERA EAVMDQLEKKVTKSEVRAKSVKAR RAEWEDLNRKTKSMFEALNEEADDNMDDAMVDDA AASKPAKRSPAPVTQTPVVEEHE GIDVDDDDIT"
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mRNA	<20272..>22263	/locus-tag="An14g05150"
CDS	20272..22263	/locus-tag="An14g05150" /EC-number="3.1.2.15" /inference="profile:COGS:COG5533" /inference="profile:COGS:COG5560" /inference="profile:PFAM:PF00443" /inference="similar to AA sequence:PIR:S67665" /note="unnamed protein product; Catalytic activity: ubiquitin C-terminal thiolester + H2O = ubiquitin + thiol. Function: UBP1 of S. cerevisiae has an ATP-independent isopeptidase activity, cleaving at the carboxyl terminus of the ubiquitin moiety in natural or engineered linear fusion proteins, irrespective of their size or the presence of an amino-terminal extension to ubiquitin. Similarity: UBP1 belongs to peptidase family C19;

also known as family 2 of ubiquitin carboxyl-terminal hydrolases. Similarity: although the predicted ORF is shorter than Ubp1 of *S. cerevisiae* and the alignment contains several gaps, it shows consistent similarity to several ubiquitin-specific processing proteases. Title: similarity to ubiquitin specific protease Ubp1 - *Saccharomyces cerevisiae*"

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 SLQSLERFLDQNV EQLGQKALLSTHQALKDIIER
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 AGPQEHVIGSGISQELQESSAGET
 RITGNQIFRNPLEGLLAQRVGCICGWTEGLSLI
 PFNCLTVPLGPKFEYDIRECLHHY
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 SLEAWETNP SVSMLSHAGRGANAG
 GHYQLRAVITHYGRHENGHYICYRKYPTDTFPAH
 VPD AII EADGDKERDERWYRLSDE
 DVQMVSEANVMSQGGAFMLFYEAVEDYSPEAAED
 VDSGLAEEEGSAPSSSCTPSETMS
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 MSDVD"

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gene	complement(<22652..>23365)	/locus-tag="An14g05160"
mRNA	complement(join(<22652..23018,23085..23287,23363..>23365))	/locus-tag="An14g05160"
CDS	complement(join(22652..23018,23085..23287,23363..23365))	/locus-tag="An14g05160"

/inference="profile:COGS:COG5126"
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 sequence:PIR:I38424"
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 Function: centrin is a ubiquitous
 component of centrosomes and
 mitotic spindle poles of diverse
 organisms and plays a role in

centrosome separation at the time of mitosis. Localization: human centrin is localized at the centrosome of interphase cells and redistributes to the region of the spindle poles during mitosis. Similarity: in the predicted ORF the EF-hands are not well conserved; this fact might have important functional consequences. Similarity: the human centrin sequence has four putative calcium-binding domains as defined by the EF-hand consensus. Title: similarity to centrin - Homo sapiens centrosome"

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AVAAAKLRSRSDDAMAAEVDAAAYRLFTRGSGGVI
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/note="unnamed protein product;
Function: thioredoxin participates
in various redox reactions through
the reversible oxidation of its
active center dithiol to a
disulfide, and catalyzes
dithiol-disulfide exchange
reactions. Similarity: the main

feature of the predicted ORF, as well as of the very similar N. crassa hypothetical protein 17E5.270, is to contain different structural domains, including the thioredoxin and the leucine zippers in the C-terminal region. Similarity: the similarity to chicken thioredoxin and similar proteins of other species is limited to a single domain of the predicted ORF. Title: similarity to thioredoxin - Gallus gallus"

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TPFGQMMKPQIEMALRGVTQGTGA
GTGTVGTQTPTTSAPTAPAQPAPVTQGSVRIASN
LAQLEHHLAAAADSCAVIFFTSAT
CPPCKMVYPTYDELAEEAGAKATLIKVDISTAMD
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WSGANPAQLRGNVRLLEMAHPPHRHQQLRLPSL
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PHHEDPRLLSMITYLKHRTSSSTPAADTPLPQDL
PSFATYLTTCGFLALDHLFALVD
LTRLLFLDPRVSGYFAEEPGHTTLLTLLSPSAGL
SGCPYNLRIVMLQLCCTLFSTPLY
RDQLTTSSSLPTLLHLTTSSLLDSHTNLRVVAA
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hypothetical As-rell1 -Halocynthia
roretzi"
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gene	complement(<27949..>28578)	/locus-tag="An14g05190"
mRNA	complement(<27949..>28578)	/locus-tag="An14g05190"
CDS	complement(27949..28578)	/locus-tag="An14g05190"
		/note="unnamed protein product; Title: weak similarity to MLL - Fugu rubripes" /citation=[55] /codon-start=1 /protein-id="CAK42080.1" /db-xref="GI:134081825" /translation="MYPFLPWSQNQSSVRSSLSE ATTSTQNVSFSSFGSSCSPTSMF PPPPPSPTDSLDDITPRKCSFSSGYEMNNSCAFP SWPNRPSLLSADSDSSTASAYLSD EDLLPIGSGSPCESAIDEESAAQDPTMGDVLTT EQQIQMIRAAAAEEEAQRARFLAQV QAHARAQQAMRVAQMAAAERENAKRKKRKAIPER KRRTASASKATVCRA"
exon	complement(27949..28578)	/locus-tag="An14g05190"
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gene	<28642..>29713	/locus-tag="An14g05200"
mRNA	join(<28642..28681, 28733..28801, 28901..29001, 29206..29402, 29446..29476, 29582..>29713)	/locus-tag="An14g05200"
CDS	join(28642..28681, 28733..28801, 28901..29001, 29206..29402, 29446..29476, 29582..29713)	/locus-tag="An14g05200"
		/note="unnamed protein product; Title: questionable ORF" /codon-start=1 /protein-id="CAK42081.1" /db-xref="GI:134081826" /translation="MGVNLGVVQSDAGMEVKKID TVWGGQDPRVEKGGVGGECINGRR ARSIGGGVWTPHLPTDKASWRTKKEPDKAARIT WNFPQCWPESKASTGNPACQARRS GGRGVFVAVRWMKQQSSWMDTREYYHCSSSGSR YVDDVGDVAAAMFELISPVRCSSSEL LKSIIGPGTKGTYLSIIMIYSHRVDSTLI"
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intron	28802..28900	/locus-tag="An14g05200"
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exon	29582..29713	/locus-tag="An14g05200"
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gene	<30773..>31030	/locus-tag="An14g05210"
mRNA	join(<30773..30823, 30902..>31030)	/locus-tag="An14g05210"
CDS	join(30773..30823, 30902..31030)	/locus-tag="An14g05210"
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		/codon-start=1
		/protein-id="CAK42082.1"
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		/translation="MLPMDVDIHPPVCMSMQLVS YQLGPKVTKMVSNAFRLFASRVGF TTHPIPSLESPSTPF"
exon	30773..30823	/locus-tag="An14g05210"
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intron	30824..30901	/locus-tag="An14g05210"
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exon	30902..31030	/locus-tag="An14g05210"
		/number=2
gene	complement(<32776..>347	/locus-tag="An14g05220"
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mRNA	complement(join(<32776. .32888,32979..33084, 33161..33253, 33402..33450, 33632..33776, 33997..34090, 34194..34227, 34305..>34762))	/locus-tag="An14g05220"
CDS	complement(join(32776.. 32888,32979..33084, 33161..33253, 33402..33450, 33632..33776, 33997..34090, 34194..34227, 34305..34762))	/locus-tag="An14g05220"
		/note="unnamed protein product; Title: weak similarity to furin-like protein 1 Furl - Drosophila melanogaster"
		/citation=[14]
		/codon-start=1

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                                STQSRGQSGMLGLHTRMRQGGEQANVSKSRKSKS
                                ISKSTGVPQNGNPEYFWKCAAEAE
                                WNAHDQLKGTQYFLLDFHPKRRTAATGAGGSCPA
                                HESYRIGKRRSPSQKGKLLLLIIYS
                                VPKRTIAGAVETIQSSTAVRSFIGGQVQRKPSL
                                TTEVWAHRQQQQQQQPQDEAIQDG
                                QINSVLVMACDGWCPSLGRSGHGIGVLVMILNSY
                                FVWDDQCQFADFHTASCSLARLTS
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exon      complement(32776..32888 /locus-tag="An14g05220"
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intron    complement(32889..32978 /locus-tag="An14g05220"
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exon      complement(32979..33084 /locus-tag="An14g05220"
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exon      complement(33161..33253 /locus-tag="An14g05220"
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intron    complement(33451..33631 /locus-tag="An14g05220"
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exon      complement(33632..33776 /locus-tag="An14g05220"
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intron    complement(33777..33996 /locus-tag="An14g05220"
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exon      complement(33997..34090 /locus-tag="An14g05220"
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intron    complement(34091..34193 /locus-tag="An14g05220"
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exon      complement(34194..34227 /locus-tag="An14g05220"
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intron    complement(34228..34304 /locus-tag="An14g05220"
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exon      complement(34305..34762 /locus-tag="An14g05220"
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mRNA      join(<35094..35340, /locus-tag="An14g05230"

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exon      35094..35340      /locus-tag="An14g05230"
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intron    35341..35442      /locus-tag="An14g05230"
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exon      35443..35474      /locus-tag="An14g05230"
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intron    35475..35525      /locus-tag="An14g05230"
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gene      complement(<35692..>374 /locus-tag="An14g05240"
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mRNA      complement(join(<35692. /locus-tag="An14g05240"
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36584..36607,
36775..36906,
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CDS      complement(join(35692.. /locus-tag="An14g05240"
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36584..36607,
36775..36906,
36960..36967,
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/note="unnamed protein product;
Title: questionable ORF"
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AIVGYMADGRKHEDYSHSHYILSA
LG GGFATPRTPARVGRLLYEPKRSVAAWNNGAHA
DIERYRKPD SRGQMDMREKDN YGV DNSK"

exon      complement(35692..35854 /locus-tag="An14g05240"
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intron    complement(35855..36342 /locus-tag="An14g05240"
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exon      complement(36343..36411 /locus-tag="An14g05240"
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intron    complement(36412..36583 /locus-tag="An14g05240"
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exon      complement(36584..36607 /locus-tag="An14g05240"

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exon complement(36960..36967 /locus-tag="An14g05240"
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exon complement(37367..37465 /locus-tag="An14g05240"
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/number=6
gene <40106..>40899 /locus-tag="An14g05250"
mRNA join(<40106..40139, /locus-tag="An14g05250"
40184..>40899)
CDS join(40106..40139, /locus-tag="An14g05250"
40184..40899)
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/inference="profile:COGS:COG1028"
/inference="profile:PFAM:PF00106"
/note="unnamed protein product;
Function: it is suggested that the
ORFL15 protein of S. spinosa is
involved in oxido-reduction during
spinosyn biosynthesis. Remark:
Spinosyns are insecticidal
microlides which are useful for
the control of arachnids,
nematodes and insects. Similarity:
SDR is a very large family of
enzymes, most of which are known to
be NAD- or NADP-dependent
oxidoreductases with different
specificities. Similarity: the
predicted ORF shows strong
similarity to several hypothetical
and described members of the short
chain dehydrogenase (SDR) protein
family. Title: strong similarity
to protein involved in spinosyn
biosynthesis ORFL15 from patent
W09946387-A1 -Saccharopolyspora
spinosa"
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PSREAMRQILDVNVVGALSTTEAFLDLLRNSSEK
RLVFVSSSTGSIIRAADPSSPFHI
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exon	40184..40899	/locus-tag="An14g05250" /number=2
gene	<41237..>43709	/locus-tag="An14g05260"
mRNA	join(<41237..41527, 41586..41762, 41850..43150, 43289..>43709)	/locus-tag="An14g05260"
CDS	join(41237..41527, 41586..41762, 41850..43150, 43289..43709)	/locus-tag="An14g05260"

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 /inference="similar to AA
 sequence:PIR:S63220"
 /note="unnamed protein product;
 Catalytic activity: ATP +
 L-cysteine + tRNA(cys) = AMP +
 pyrophosphate +
 L-cysteinyl-tRNA(cys). Similarity:
 YNL247W of *S. cerevisiae* belongs
 to class-I aminoacyl-tRNA
 synthetase family. Title: strong
 similarity to cysteine--tRNA
 ligase YNL247w - *Saccharomyces*
cerevisiae"
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 DYFKFDVEFVMNITDVDDKIILRG
 RQQHLFNKYIAEHPTVTPDVLETARKAYSAYIKK
 NLPLVDPDTEPENFVAEAQKTVTA
 TTSAIAEAAQKLAGIDAASSKAFYDAAQDVFCFY
 LDVTEGSTIPGDAHEIFTKLTKKY
 EDHFMRDMRDLNVLPDAVTRVTEYGQQIADFVE
 KIVANKFGYVTS DGSVYFDIKA FE
 EAGNHYARLEPWNRNNQPLLRDGEGLSRATEKK
 SSDDFALWKASRPGEPSWSSKWGQ
 GRPGWHIECSAMASSCLGSQIDIHSGGIDLAFPH
 HDNELAQSEAYWCEHKQQWVNYFL
 HMGHLSIQGSKMSKSLKNFTTVKDALERG DYTPR
 SLRIVFLLGGWRDGEITDDL IKN
 ASSWEEKLNNFFVKAKDPSSFRSSDEAPTSSSET
 LSQALKSTQEKVHEYFCDSFDTPK
 VMAAISELVTTFNALDSQTLDLKVVESMGTWVTQ
 IVTIFGLNGAASSDSCGIGWEGTD
 IPEAAKRFLYPLSAMRDTLRQAAILDDTKQASKD
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		NKPALVRPVTKDMLQAREEQARKALLKQQEKEKQ EKLAQERLEKGKLNPNVEMFRTSEY SAWDEDGIPTKDAAGEPLAKSKSKKLRKDWERQK KAHEAWLASQNGK"
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intron	41763..41849	/locus-tag="An14g05260" /number=2
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gene	<43954..>45254	/locus-tag="An14g05270"
mRNA	join(<43954..43984, 44194..44823, 44878..45059, 45108..>45254)	/locus-tag="An14g05270"
CDS	join(43954..43984, 44194..44823, 44878..45059, 45108..45254)	/locus-tag="An14g05270" /codon-start=1 /product="hypothetical protein" /protein-id="CAK42088.1" /db-xref="GI:134081833" /translation="MALDNARRVYIQLNNIDLHT ITTDLSRLHVQRLMRLTAKQASDI RELSICSASGGPLSLGYRVLPSCPLKSQASKDLR EALKKKLKQCRTLRI SAVEIKHTDY ELAWMGAIDMTHSVLSAFCETQNSLKS LTLD FRT DNVASLLRGGLERIPSYGPAELSR FPFGSSRINHISLNLNANIAGSPGLCERLLHPLY TRYGVNEVSLDLGKAYAENVVLDV LRGMGHRMLEPKLKQYCHSLRVLT MENIIFRYNY WLRFLHSLKREFRRLQEVNLFWEV NTSSESTSLITQWNHNTIYDNTQTRV TYTGPEEH GALTALEKIAS EDPLSVHL"
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intron	44824..44877	/locus-tag="An14g05270" /number=2
exon	44878..45059	/locus-tag="An14g05270" /number=3
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exon	45108..45254	/locus-tag="An14g05270" /number=4
gene	<46541..>47683	/locus-tag="An14g05280"
mRNA	join(<46541..47034, 47092..47344, 47501..>47683)	/locus-tag="An14g05280"
CDS	join(46541..47034,	/locus-tag="An14g05280"

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47501..47683)

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gene	<48251..>50618	/number=3
mRNA	join(<48251..48422, 48475..>50618)	/locus-tag="An14g05290"
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SKQPNKKSPDENS LGYAGRAMPCPSTVALMHYPL
ILDLFREKYATSVRKGFCLDSLTT
LRECGATSKGKWKQPGLELAEKLSTERWQILRI
LEDLEHEVPHAVCDIRQNIQVDRK
KGLTVAEVKAIMRVMAVRIGLDCYRPHFLMPTLM
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/inference="similar to AA
sequence:UniProtKB:SPBC29B5.2"
/note="unnamed protein product;
Function: isp4 of S. pombe is a
membrane oligopeptide transporter.
Remark: isp4 of S. pombe was
originally identified by
subtractive screening as gene
induced during the sexual
differentiation process.
Similarity: the predicted A. niger
protein shows strong similarity to
protein isp4 of S. pombe, which
belongs to the OPT subfamily of
transporters specific for small
oligopeptides (from the C.
albicans OPT1 gene). Title: strong
similarity to protein isp4p
-Schizosaccharomyces pombe plasma
membrane"
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		HIVSLVAELLAYPCGVFLAKVLPLWTISLGRGLGS FTLNPDRHFNIKEHALIVIMSNVS FGYGSADSTNIIQASSARFYNFGLSAGFSVLVVL CAQLLGFGVAGLAAPWLVEPARII WPQVLSNCAMLETLHSRANTVANGWKISRLRFFL YVTAGGFVWYFFPGLMFTALSYFT WICWIAPRNVVVNQLFQMOTGLGLSPITFDWSQV AYNTNPLLSPSWAAINVFAGFALF FWIVVPGIYYSNWFTAYLPLMTADVYDRTGTVY DTARVISADNTLDVDAYRQYSPPY LPATYAFVYGLSFASITAVLTHIGVWHGKEVWAA LKGKNKLDIHARLMKSYKKTPWYW YAAIIAIIITAIAIVMVEVYHTKLPVYGVLGLII PAIYMVPCGIIQGITNVDANQLNV LAEFIGGYMFEGKPLANMIFKILSTDVVGQGVYF AMDMKLGHYLKIPRTLFMQAQGLA TILGALTQAGVTIWMLGHIQDICSSDQSDGFTCP NGRTVYSSSVIWGLVGPRRLYSVG RIYSSLLHFFWIGAIAPLITYFLYKYTRKQFWKY INWPLIFVGTYNVPPATGINYSSW ALVNFAFNHFIKKRFFAWKKYNYILAAALDTGL ALSGIVIFFCISYPGAVFPDWWGN TVYVNTADGEGVAYKSMPEVGYFGPANGTWS"
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intron	48423..48474	/locus-tag="An14g05290"
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exon	48475..50618	/locus-tag="An14g05290"
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gene	complement(<51277..>53277)	/locus-tag="An14g05300"
mRNA	complement(join(<51277..51279,51332..51599,51656..51726,51783..51947,52973..53002,53059..>53277))	/locus-tag="An14g05300"
CDS	complement(join(51277..51279,51332..51599,51656..51726,51783..51947,52973..53002,53059..53277))	/inference="profile:COGS:COG0724" /inference="profile:PFAM:PF00076" /inference="similar to AA sequence:SWISSPROT:YRA1.YEAST" /note="unnamed protein product; Complex: YRA1 of S. cerevisiae mediates nuclear export of mRNA by interacting with several other protein factors, like Mex67. Function: YRA1 of S. cerevisiae is an mRNA-binding protein involved in the nuclear export of mRNA towards the cytoplasm. Remark: although the gene structure looks strange,the strong similarity to known proteins justify the model. Similarity: YRA1 S. cerevisiae belongs to the evolutionarily conserved REF (RNA and export

factor binding proteins) family of
hnRNP-like proteins. Title: strong
similarity to RNA annealing
protein Yra1 - Saccharomyces
cerevisiae nucleus"

/citation=[36]

/citation=[67]

/citation=[68]

/citation=[86]

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12)

mRNA complement(join(<54264. /locus-tag="An14g05310"

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/feature=1
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Function: the S. cerevisiae
homolog Did3p is a class E Vps
factor, which function in the
maturation of a late
endosome/prevacuolar compartment
into multivesicular bodies that
then fuse with the vacuole.
Remark: DID3 of S. cerevisiae is
also called YKL041w. Remark: S.
cerevisiae Did3p is probably
involved in the ubiquitin-mediated
maturation of multivesicular
bodies. Title: strong similarity
to protein involved in vacuolar
protein sorting Did3 -
Saccharomyces cerevisiae endosome"
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MRQLSTELVRAGIIEEMVDDAIPN
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PEKPLEEAPEPEDEFADQEATLEQ
MRGRLEALKS"
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/number=2
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CDS       join(55690..55720, /locus-tag="An14g05320"
55913..56238,
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sequence:PIR:T39220"
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Function: WOS2 of S. pombe is a
cochaperone protein that interacts
with cdc2 in the control of the
M-G1 transition. Similarity: WOS2
of S. pombe belongs to the p23 /
wos2 family. Title: strong
similarity to cell cycle regulator
p21 protein wos2p -
Schizosaccharomyces pombe"
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		NETYKQALDTLHDAFNARTRDSEG
		AFWYFNPYPNWGVLEGLYPLGSFISMWKTYFEPT
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		FMTLVDLLERSGKNSAILNETQRD
		DVYTKYWNVANTIINDADEETGCWWQVMLHGEE
		GNYIESSGSAQFVYGLLKGARLGY
		LQGKTPNGVGYTDAADKCYNLVSEFVKEEADGS
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exon	61367..61434	/number=3 /locus-tag="An14g05340"
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exon	61480..61522	/number=4 /locus-tag="An14g05340"
gene	complement(<62253..>63796)	/number=5 /locus-tag="An14g05350"
mRNA	complement(join(<62253.. .62358,62418..62491, 62545..62677, 62734..63473, 63541..63615, 63704..>63796))	/locus-tag="An14g05350"
CDS	complement(join(62253.. 62358,62418..62491, 62545..62677, 62734..63473, 63541..63615, 63704..63796))	/locus-tag="An14g05350"

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 Function: ayg1 of A. fumigatus has
 an unknown function, but it is
 contained in the gene cluster
 responsible for conidial
 pigmentation. Phenotype: ayg1 null
 mutants of A. fumigatus have
 yellowish-green conidia. Title:
 strong similarity to hypothetical
 yellowish-green 1 ayg1 -
 Aspergillus fumigatus"
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 PADPSDPESADRQWTTVLDMATRPEFDMSRVAA
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 shows very strong similarity to
 abr1 of A. fumigatus, a gene of
 the conidial pigmentation gene
 cluster; abr1 mutants have brown
 conidia, and the proposed function
 of abr1 is multicopper oxidase.
 Title: strong similarity to cell
 surface ferroxidase precursor Fet3
 - Saccharomyces cerevisiae plasma
 membrane"
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gene	complement(<67552..>687 35)	/locus-tag="An14g05380"
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 Title: weak similarity to
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- Homo sapiens"
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QNTEAWKKNFSSSEAGLRRVDLLLEGIQKWARANP
DTWRKEAIRAGLKTALFAFVGLML
GDGIAGANDINHMMSDSRLKGLWAEARKRRDEL
GHVTTGKMPPPVPTTPAPRPTGQE
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Similarity: SDR is a very large
family of enzymes,most of which
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with different specificities.
Similarity: the predicted ORF
shows strong similarity to several
hypothetical and described members
of the short chain dehydrogenase
(SDR) protein family. Title:
similarity to meso-2,3-butanediol
dehydrogenase (D-acetoin forming)
budC - Klebsiella pneumoniae"
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CDS	82379..83449	/locus-tag="An14g05440" /note="unnamed protein product; Title: strong similarity to hypothetical protein encoded by An11g07600 - Aspergillus niger" /codon-start=1 /protein-id="CAK42105.1" /db-xref="GI:134081850" /translation="MDTDKAAETTRLHEENEDPA VKDVIRVASYHRLDYDLAVIRTFP RPHHLIRDLLTPKTLIIDLNSRLGVLDVFPLEFI HEICLMLDVQSLFRFHRVNRARQ IASASGYKAVVKAIGALFVILRTGMASWYKLS DLYDVLCTKNCAICNDFGGFIFLP SFMRCFFFCIEDDELPPVLPASQVRPYLNRRSAP PLSSRIPMIKTLPGIYSLDESKRT RRFELVLEQSAISLFSSDRVPTFPKKYSRDTLQ RYMVSTALPYLDNKNVDVIEKGVSC SGCQISLEKALQSSGAEYDVWDDRDKIYSHDQFM EHFETCPEARKLWELSEGGTIEPD IPAFVKNGGCAKKRELKNVFIYH"
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CDS	complement(join(87776..88536,88589..89339))	/locus-tag="An14g05470"
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		SSTPRDPRSSFVLVLRTRFQDHAS
		TAEMEGFLFGHIYHCSRLRLMSRDDIVTTAAS
		THPNNQPGSQPGSQSKIPQGSCAG
		IFTYRSSICESDIEILTTEDSHTVHYANQPDYDP
		ISDTLIPGASSIVNLTKPWTSWTT
		HRLDWVADMSAWYADGQLQSKSNYSVPDRPSIVA
		MNLWSNGGNWSGDMKVGESVFMGI
		EWIELVYNVTKADQDLPIKDHPGHRDRYHRVGGL
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LLFLLFFFFFFFFFPSPITHLPIT
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SRLLLTMSGVFSTM RPSVEDHPMP
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involved in regulating ceramide
and phosphorylated sphingoid base
levels, and modulates stress
responses through sphingolipid
metabolites. Remark: YSR3 of *S.*
cerevisiae is also called YKR053c.
Similarity: *A. niger* EST
EMBLEST:BE760128 comprises part of
the putative 5'-UTR of the gene
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		of its recently identified	

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functions is the regulation of
beta-1,3-glucan synthase, which
synthesizes the main component of
the fungal cell wall. Similarity:
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CDS	join(127622..127779, 128125..128227, 128313..128417)	/locus-tag="An14g05660"
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exon	128313..128417	/locus-tag="An14g05660" /number=3
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mRNA	join(<134201..134238, 134452..134502, 134768..134993, 135113..>135346)	/locus-tag="An14g05690"
CDS	join(134201..134238, 134452..134502, 134768..134993, 135113..135346)	/locus-tag="An14g05690"
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		/number=3
exon	135113..135346	/locus-tag="An14g05690"
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mRNA	6476) complement(join(<135466	/locus-tag="An14g05700"
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	136059..136189,	
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CDS       complement(join(137703. /locus-tag="An14g05710"
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/note="unnamed protein product;
Similarity: although the
similarity to Rhp16 of S. pombe is
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ORF suggest that it might be
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repair. Title: weak similarity to
RAD16 nucleotide excision repair
protein homolog rhp16p -
Schizosaccharomyces pombe"
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/inference="similar to AA
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required for appressorium
differentiation in response to
inductive surface cues. Function:
as do most fungal plant pathogens,
M. grisea differentiates an
infection structure specialized
for host penetration called the
appressorium. Phenotype: M. grisea
cells null mutant for PTH11 are no
more pathogenic. Similarity: the
length of the predicted ORF is
only one half of the M. grisea
PTH11. Title: similarity to
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YGLLGCLCIYYIVAEIVKIRMCDPVPAYWTQDPK
ARCLNQRAALIADSVISVVTDFII
LILPLPLTWSLQMSRNKKLRVIGMLSAGGLATAF
SLYRLVLVLRDGSSRDQTIVFMIV
ILSGNAEGGVAMICACLPVNIINKLRKKEYSS
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gene	complement(<145510..>146577)	/number=3 /locus-tag="An14g05760"
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53)
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gene      complement(<147404..>147784) /number=6 /locus-tag="An14g05765"
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CDS       complement(147404..147784) /locus-tag="An14g05765"
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CDS       join(149275..150089, /locus-tag="An14g05780"
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          150521..150765)
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          /inference="profile:PFAM:PF01222"
          /inference="similar to AA
          sequence:PIR:S64014"
          /note="unnamed protein product;
          Function: the S. cerevisiae ERG4
          gene encodes sterol C-24(28)
          reductase which catalyzes the
          final step in the biosynthesis of
          ergosterol. Remark: ergosterol is
          the precursor of vitamin D2.
          Title: strong similarity to sterol

```

		C-24 reductase Erg4 - Saccharomyces cerevisiae endoplasmatic reticulum" /citation=[6] /citation=[18] /citation=[22] /citation=[54] /citation=[66] /codon-start=1 /protein-id="CAK42139.1" /db-xref="GI:134081884" /db-xref="GOA:A2R3X1" /translation="MKQSKDRSPEGTSNAHEDEK PTFEFGGAPGVTMLMLGFLLMY MFIGATLYDGHLPLPDENQSITDFLSHLVLAHT HAYPNRKAWIIYWTFLVLEGLGYL YLPGVYKGKCLPHLNGKQLDYYCSAASSWYVTI AAALVLHFGIFRLSTLVEEFGPL MSVAICSGFLVSI IAYVSALLRGAQHRMTGSHVY DFFMGAELNPRLFQWLDKMFEEV RIPWYILFLLTLGTALKQWEDYGFSGEVSFLLL AHFLYANACAKGEELIITSWDMYY EKWGFMLIFWNLAGVPMSYCHCTLYLASHDPSTY KWNPIALGVLFVMIYIFAYWVWDT NSQKNLFRAQERGKPVNRKTFPQLPWKSVKNPVC IKTKTGDSILCSGWYGMARKVHYS CDWFFAFSWGLITGFNSPFPWFYSCFFTVMIIHR ALRDIERCRCRERYGEAWREYERRVP YLFIPVSRLELVL"
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exon	150140..150471	/locus-tag="An14g05780" /number=2
intron	150472..150520	/locus-tag="An14g05780" /number=2
exon	150521..150765	/locus-tag="An14g05780" /number=3
gene	complement(<151141..>153445)	/locus-tag="An14g05790"
mRNA	complement(join(<151141..151564, 151613..151848, 151899..152339, 152378..152673, 152720..153109, 153190..153256, 153395..>153445))	/locus-tag="An14g05790"
CDS	complement(join(151141..151564,151613..151848, 151899..152339, 152378..152673, 152720..153109, 153190..153256, 153395..153445))	/inference="profile:PFAM:PF04082" /note="unnamed protein product; Similarity: the predicted protein shows similarity to several putative and described fungal transcription factors; their

common feature is the presence of a typical binuclear cluster zinc-finger, responsible for DNA binding, which is not well conserved in the predicted protein. Title: weak similarity to transcription activator prnA - *Aspergillus nidulans*"
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EQRSASIERLSSDLMTVRDKLLAIDVSRGLYADS
LHGMAACADFIAYSVLTVIYRAQT
HPRDVM AVSSQCYASATAALQSHLKCF TYFRGRQ
THKQTEYVNWILLYPSFTPFVIVF
THAITTASTADLALLQDTASSLELIKGLSRGSMH
LYTICDAFVRAAQILVNSQQTLTG
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intron	complement(152674..152719)	/number=4 /locus-tag="An14g05790"
exon	complement(152720..153109)	/number=4 /locus-tag="An14g05790" /number=5

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		/locus-tag="An14g05800"
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CDS	154037..156562	/gene="aguA"
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		/inference="profile:PFAM:PF03648"
		/inference="similar to AA sequence:UniProtKB:ANI290451.1"
		/note="Function: hydrolysis of alpha-D-1,2-(4-O-methyl)glucuronosyl links in the main chain of hardwood xylans. Gene-ID: aguA"
		/citation=[58]
		/codon-start=1
		/product="alpha-glucuronidase aguA-Aspergillus niger"
		/protein-id="CAK42141.1"
		/db-xref="GI:134081886"
		/db-xref="GOA:A2R3X3"
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exon	154037..156562	/gene="aguA" /locus-tag="An14g05800" /number=1
gene	<157327..>158616	/locus-tag="An14g05810"
mRNA	join(<157327..157515, 157564..>158616)	/locus-tag="An14g05810"
CDS	join(157327..157515, 157564..158616)	/locus-tag="An14g05810" /EC-number="2.3.1.48" /inference="profile:COGS:COG5076" /inference="profile:PFAM:PF00439" /inference="similar to AA sequence:PIR:S28051" /note="unnamed protein product; Complex: GCN5 of S. cerevisiae is a component of the SAGA complex, which possesses histone acetylation function and is important for transcription in vivo. Function: GCN5 of S. cerevisiae and many other organisms acetylates histones H3 and H4 non-randomly at specific lysines, causing chromatin remodelling during transcriptional activation. Similarity: in the C-terminal part of the protein there is a bromodomain, which function may be to tether type A histone acetyltransferase to the chromatin during gene activation. Title: strong similarity to histone acetyltransferase Gcn5 - Saccharomyces cerevisiae nucleus" /citation=[21] /citation=[23] /citation=[29] /citation=[31] /citation=[34] /codon-start=1 /protein-id="CAK42142.1" /db-xref="GI:134081887" /db-xref="GOA:A2R3X4" /translation="MDGAELQSPLLDNGQPPLVA KRVTSEEPNAAADAKRLKTSDDRE APPQTNLPAATRIVPFPEKPAVVEERNCEIEFRV VNNDGSTESTVILTGLKNLFQKQL PKMTKDYIARLVYDHTLHLAICKMPLEIIGGIT FREVRHRRFAEIVFCAASSDQQVK GYGAHLMAHLKDYVRATSPVMHFLTYADNYATGY FQKQGFTKEITLDKSIWMGYIKDY EGGTLMQCSMLPRIRYLEVGRMLLKQACVLAKL

		RPLSRNHIVHPPPPQWANGIVTLI DPLSIPAIRATGWSPDMDELARQPRHGPHFNELR RFLSKIQAHKQAWPFLSPVKNDEV PDYYNFIESPMDLSTMEERLENDTYSTPKELIND LKSIFRNCRQYNDATTIYAKSATK LEKYIYSLIKEVPEWFDLVKE"
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intron	157516..157563	/locus-tag="An14g05810" /number=1
exon	157564..158616	/locus-tag="An14g05810" /number=2
gene	<159715..>163074	/locus-tag="An14g05820"
mRNA	join(<159715..160332, 160378..160543, 160593..160722, 160785..160893, 160962..162768, 162857..>163074)	/locus-tag="An14g05820"
CDS	join(159715..160332, 160378..160543, 160593..160722, 160785..160893, 160962..162768, 162857..163074)	/locus-tag="An14g05820" /EC-number="3.2.1.23" /inference="profile:COGS:COG1874" /inference="profile:PFAM:PF01301" /inference="similar to AA sequence:UniProtKB:A00968.1" /note="unnamed protein product; Catalytic activity: hydrolysis of terminal,non-reducing beta-d-galactose residues in beta-d-galactosides. Function: cleaves beta-linked terminal galactosyl residues from gangliosides, glycoproteins, and glycosaminoglycans. Remark: beta-galactosidase of A. niger has been already patented under patentnumber WO9010703 and WO9716555-A1. Similarity: belongs to family 35 of glycosyl hydrolases. Similarity: the absence of nice BLASTN alignments,demonstrates that the predicted ORF is just an homologue of the already described beta-galactosidase of A. niger. Title: strong similarity to beta-galactosidase lacA - Aspergillus niger extracellular/secretion proteins" /citation=[9] /codon-start=1 /protein-id="CAK42143.1" /db-xref="GI:134081888" /db-xref="GOA:A2R3X5" /translation="MKTSFLLAIGLAVEACLGLV SAPNYVRQINATDSSLQDIVTWDE YSIRVRGERILLLLGEFHPFRLPCPGLWLDFVQK

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 VSGGGFPGWLKRVQGRCLKTTDQGY
 LDAITPYMQAIGRIIAKAQITNGGPVILFQPENE
 YTACVQDEGYTQKEYMAYVEEQYR
 KAGIVVPFIVNDADPMGNFAPGTGVGAVDIYSFD
 DYPLQWSTAPSNPSNWSSLISPLL
 SYNETVHEEQSPTTFFSISEFQGGVPDAWGGVGI
 ETSAAAYIGPEFERIFYKINYGFRA
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 VRHGELTSRESTSYKLRVNTSAGN
 LAIPQLSGSLSLHGRDSKIHLDYDYNVGNVSLIYS
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 AYNWVLDLVPVGAIGHVSRSHNRSVIVKAGY
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 YHKPNISLPDLTTLDWYYLNTLPE
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 DYGNGGTLTYRGFTATGNETSL
 YLLTEGGYAYGHSIWLNNTFLASWPGNPAFLLSN
 QTITFPSPLTPGTTYKLTLIDHL
 GNDENFPANGFEMKDPRGILDYTLHGRDDKSAIS
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exon	162857..163074	/number=5 /locus-tag="An14g05820"
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CDS	complement(163244..165037)	/locus-tag="An14g05830"
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CDS       complement(join(166037. /locus-tag="An14g05840"
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          /note="unnamed protein product;
          Catalytic activity: A. flavus omtB
          converts demethylsterigmatocystin
          (DMST) to sterigmatocystin (ST)
          and
          dihydrodemethylsterigmatocystin
          (DHDMST) to
          dihydrosterigmatocystin (DHST).
          Function: A. flavus omtB is a
          demethylsterigmatocystin
          6-O-methyltransferase involved in
          aflatoxin biosynthesis. Remark:
          aflatoxins are polyketide-derived
          secondary metabolites. Title:
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          PEFLRMTNFGQNP SGAVKGALQYAEKTEM SLWDWV
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          LEWFPVKERIIDGFHQGESNVLLVDVAGGRGHDL
          VAFESKFSEVQGR LILEDLPHVVA
          EATQHPKIEHVSFDLFQAQPIQGARTYYMKFILH
          DWSDEESRQILSHLAAAMKMGYSK
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exon	complement(167142..167268)	/number=3 /locus-tag="An14g05840"
intron	complement(167269..167318)	/number=4 /locus-tag="An14g05840"
exon	complement(167319..167516)	/number=4 /locus-tag="An14g05840"
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CDS	join(168480..169074, 169128..169245, 169293..169453, 169507..169540, 169597..170002)	/locus-tag="An14g05850"

/note="unnamed protein product;
 Function: PTH11 of M. grisea is
 required for appressorium
 differentiation in response to
 inductive surface cues. Function:
 as do most fungal plant pathogens,
 M. grisea differentiates an
 infection structure specialized
 for host penetration called the
 appressorium. Phenotype: M. grisea
 cells null mutant for PTH11 are no
 more pathogenic. Similarity: the
 similarity to PTH11 of M. grisea
 is limited to the N-terminal half
 of the predicted ORF. Title:
 similarity to integral membrane
 protein PTH11 - Magnaporthe
 grisea"
 /citation=[63]
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 IEAFKYTVIAPNFSMVSTTTGKLSVAVFLLRLMG
 QTASPAKRWFLYIFSIIISVAVNNVL
 AIVAIMGYCRPAEKIWRPEVPGSCFSLKFQLIAG
 ISQASFNAFADLTALFPPIIFWS
 VQLPWKMKLGVIAMGAGILAAAATLVKAILLKS
 LPAHSDITCEHQIRGRAQTHKKKL

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intron	169454..169506	/locus-tag="An14g05850" /number=3
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intron	169541..169596	/locus-tag="An14g05850" /number=4
exon	169597..170002	/locus-tag="An14g05850" /number=5
gene	<170380..>172035	/locus-tag="An14g05860"
mRNA	<170380..>172035	/locus-tag="An14g05860"
CDS	170380..172035	/locus-tag="An14g05860" /codon-start=1 /product="hypothetical protein" /protein-id="CAK42147.1" /db-xref="GI:134081892" /translation="MACPPTATCPIISSSLVTKS AFKSKETRENGSESESERNSQHIA KSTGNANAELQQTGKVKELFQDYGHGRSPESITV GGAYAPMSGYFLPSNLLEDQNGPR TPKIIAEGLAVPAGKVKGDDSEPVSAMVTSRMK LNQVLGNRRKVGCAASLPAGTAAH PVEHGPLAGRSSGVGVSFGEAGDPAFEGSYEDDY DDACANHAASDGDREDKEALKNGG KTDNTGESEYPRFSQVDYFTQHQSLQIRTTGLPK RPRYSAATVGFPCPVTWAFIDRG DPKHGMPTAADLPWEIRTLHETNELNTIAAYLAS MRRNLKDLVDNFTFHYRPVSFIDK ADRVKKIGGYSSDKQNAHTVADLYMHTKDDRSW GTLCVTREHHVQGMWHYWAFAAI SPPKSPFQSVDEKGVYLLMYDSRPLKEPTKKRDR DYWRNYMRRDQYKLLVEIGKNFKV LDLAINRRQLSVEGEDDPLRLTLWWLWNIARYGG GFYERDGELEDDPRWRLTDARWLHF DQDWSSNVRTALRWKNVKEWFSEQRLDEQLTHEQ RIQAHAVAA"
exon	170380..172035	/locus-tag="An14g05860" /number=1
gene	<172769..>173936	/locus-tag="An14g05870"
mRNA	join(<172769..172958, 173013..173080, 173134..173513, 173575..173639, 173698..>173936)	/locus-tag="An14g05870"
CDS	join(172769..172958, 173013..173080, 173134..173513,	/locus-tag="An14g05870"

173575..173639,
173698..173936)

/note="unnamed protein product;
Function: PTH11 of M. grisea is
required for appressorium
differentiation in response to
inductive surface cues. Function:
as do most fungal plant pathogens,
M. grisea differentiates an
infection structure specialized
for host penetration called the
appressorium. Phenotype: M. grisea
cells null mutant for PTH11 are no
more pathogenic. Similarity: the
length of the predicted ORF is
only one half of the M. grisea
PTH11. Title: similarity to
integral membrane protein PTH11 -
Magnaporthe grisea"

/citation=[63]

/codon-start=1

/protein-id="CAK42148.1"

/db-xref="GI:134081893"

/translation="MTPLNHWGITLVVPIVACV

VTTLFFILRLYSRRLVRQKLDLGD

VLMGIGLFFSYGLTLCTVISAFNGVGHEFWLSLR

PTRGTVTLLFWCSTKFWVLSHV

KFSYIVLLRKLFGAITYWRRLLTALIVFTLAWGI

ASIFVSIFQCWPVRYFWIKHIDGS

CMQGRNTFYIVVGSIALAENFILVSMPLVVVWGM

NLSPRQKVELSLIFGFGGLVCAIG

LLRMVTFKRYVTADATTNGYLQAIWSIVELELGI

ICASVILMRPIFQPPLGIIQNEML

HHAWPNIKVQLLFKRRADDEFVMAEAAGLCRDG

ISG"

exon 172769..172958

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intron 172959..173012

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/number=1

exon 173013..173080

/locus-tag="An14g05870"

/number=2

intron 173081..173133

/locus-tag="An14g05870"

/number=2

exon 173134..173513

/locus-tag="An14g05870"

/number=3

intron 173514..173574

/locus-tag="An14g05870"

/number=3

exon 173575..173639

/locus-tag="An14g05870"

/number=4

intron 173640..173697

/locus-tag="An14g05870"

/number=4

exon 173698..173936

/locus-tag="An14g05870"

/number=5

gene <175066..>176514

/locus-tag="An14g05880"

mRNA join(<175066..175356,

/locus-tag="An14g05880"

175420..175941,

176025..176078,

176188..>176514)

CDS join(175066..175356,

/locus-tag="An14g05880"

175420..175941,

176025..176078,

176188..176514)

		/inference="similar to AA sequence:UniProtKB:NCB9I2.2" /note="unnamed protein product; Similarity: the central part of the predicted ORF shows only weak similarity to N. crassa B9I2. 20. Title: strong similarity to hypothetical conserved protein B9I2.20 - Neurospora crassa" /codon-start=1 /protein-id="CAK42149.1" /db-xref="GI:134081894" /translation="MPLASDAFQADLSRLSPSHL EVSLPVTLSLAVLAYLLLVSTLRF QRVRILYRDYPQYTTTRASMSQMTVDDAWAIQKNI LQLEFPTTAVKALQFALFRTYGIP TISSLLLHTSQFSNPATSFKRYADTGALIGQFVT CPPTSSRARTAIARTKFLHSGYRA SGRILESDMLYTLSLFATEPIRFVERFEWRAMTE LERCAIGTYWKS LGDALDISYDEL PSGKSGFSDGLHFLEELRQWGDHYEENMRPDHR NRLVADKTMDVIVYGFPKWHILCD GFCKEPCADSLNQEVFSDTPNEDGRYYVQIWKGM PYYVQPTMWNRWGPAAWLTWALGL PLPGDDGDTYYPRGFDVADLGPRQFEGRGRKSVG EYVDVLEKEHKGQCPFGGRSDQPE ICLSR"
exon	175066..175356	/locus-tag="An14g05880"
		/number=1
intron	175357..175419	/locus-tag="An14g05880"
		/number=1
exon	175420..175941	/locus-tag="An14g05880"
		/number=2
intron	175942..176024	/locus-tag="An14g05880"
		/number=2
exon	176025..176078	/locus-tag="An14g05880"
		/number=3
intron	176079..176187	/locus-tag="An14g05880"
		/number=3
exon	176188..176514	/locus-tag="An14g05880"
		/number=4
gene	<176803..>178484	/locus-tag="An14g05890"
mRNA	join(<176803..177362, 177419..>178484)	/locus-tag="An14g05890"
CDS	join(176803..177362, 177419..178484)	/locus-tag="An14g05890"
		/EC-number="5.2.-.-" /inference="profile:COGS:COG4716" /note="unnamed protein product; Remark: CLA compounds(cis,trans)-9,11-linoleic acid and (trans, cis)-10,12-linoleic acid are recognised nutritional supplements and effective inhibitors of epidermal carcinogenesis and forestomach neoplasia; furthermore CLA has also been shown to prevent adverse effects caused by immune stimulation in chicks, mice and rats, and has been shown to decrease the ratio of low density lipoprotein cholesterol to high

density lipoprotein cholesterol.
 Remark: the linoleate isomerase is used in a method for producing conjugated linoleic/linolenic acid (CLA) from oils such as sunflower oil, safflower oil, corn oil, linseed oil, etc. Similarity: the N-terminal part of the prediction ORF shows also weak similarity to some oxidoreductases. Similarity: the patented protein, as well as the predicted ORF, show strong similarity to the 67 kDa myosin-crossreactive streptococcal antigen of Streptococcus pyogenes, a protein with unknown function, but involved in the pathogenesis of streptococcal infections.
 Title: strong similarity to linoleate isomerase protein sequence PCA591 from patent WO9932604-A1 -Lactobacillus reuteri"

/citation=[19]
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 DAWILGAGISSLTAAVHLIQEAHV
 PPSRVHILETLSQAGGGSISTGDPVNGYDCRAGG
 MPPFNDVCMEEELSLVPSKTNPNL
 TVLEEFHEFWDEAVKDHPTFLTRHKHGLERI
 DAKRASLGLRDRVDFMLASKSDK
 SLGRSRICDHFNSFFKSYWMLLSTTFGIKPVH
 SAAEFRRLQHYMHDIHEIHCRK
 LDGGRYNRHESIVSPIAHFLCSRGVDVFRFHTTVT
 DIITTPSSSEPHRVSAIKAIHENE
 PEMTINLGERDIVLVSLGSMMSGSTTGNTSPPS
 LELMDIEKDLDENWLLWLELSTKN
 PIFGNAYNFCTRMAESRLESFTVTFSSPEFFNRF
 TALTGDKVSGTFVTLKDTPWLLS
 INLPQQPLFPDQPAHVQVLWGYAMPERE
 GDIK
 KPMLECSGQEIMEEILKQLNFPVQ
 GILDHSITLPCVVPRAAATLLVRLRSDRPPVIPP
 GIDNLGLIGQFVDIPGEVAVTMDY
 GVRSAQTAVRQLMGLERHKVLSKRSSAINLKAL"

exon	176803..177362	/locus-tag="An14g05890" /number=1
intron	177363..177418	/locus-tag="An14g05890" /number=1
exon	177419..178484	/locus-tag="An14g05890" /number=2
gene	complement(<179356..>181260)	/locus-tag="An14g05900"
mRNA	complement(join(<179356..179403, 179482..>181260))	/locus-tag="An14g05900"
CDS	complement(join(179356..179403, 179482..181260))	/locus-tag="An14g05900"

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/inference="profile:COGS:COG3122"
/inference="similar to AA
sequence:PIR:T49456"
/note="unnamed protein product;
Similarity: other BLASTP hits are
explained by the relatively high
content of low-complexity regions.
Title: strong similarity to
hypothetical protein B14D6.80 -
Neurospora crassa"
/codon-start=1
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/db-xref="GI:134081896"
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QLSIRRAHSHPPVPASDSIFSDE
IDLSAFTYDNP IEQPAKRRRLSHEITPVKDVPLP
PAKNSLFLFSDDDIILSSDGPAPT
KPPAWNGESDPIVFTSSAPEPTHNLPVRPAISSR
AVNTISLDDDDAGNSSDTRSNRP
RKEAIQVSSDQLDFPDVDDLDDVAQRVEANAFSS
RTANLLATLEDRSRGNGESASRS
SRGRRIQDQSDDIEVEEMPPPRKPQRKAIKVTSE
EKEAKAREREAAKAQREHDRQLEK
ERKQKAKEDKAREKQLAADIAEVNKLKVDKKDST
HEMLIDLASTFTDTS LGNQTS ELM
RLKVDLSFFPSTIPNIVKWRKVRATYNDLSLGH
WEPCALHIRDEEEHVLCLIAAQDF
INMIVAPTTEPRNTINDHVERLKLAYPKSRPIYL
IEGLTSLMRKNNNAQNRAYQAAVR
RQYEDSSARPSTRKQQQPEPVTPIDSDTVEDAL
LDLQVTHSCLIHHTSSPAESAEWI
KNFTEYISTVPYRRERMDLNSAFCMDVGQVKPG
ENRSDAFVKMLQEVNVRTASMAYG
IATQYPSAMDLVNAMRKHGPGLLDVKQTKTAPS
PIHALVQP"

exon      complement(179356..1794 /locus-tag="An14g05900"
03)

intron    complement(179404..1794 /locus-tag="An14g05900"
81)

exon      complement(179482..1812 /locus-tag="An14g05900"
60)

gene      complement(<181479..>18 /locus-tag="An14g05910"
2990)

mRNA      complement(join(<181479 /locus-tag="An14g05910"
..182086,
182177..182601,
182623..>182990))

CDS       complement(join(181479. /locus-tag="An14g05910"
.182086,182177..182601,
182623..182990))

/EC-number="2.4.1.-"
/inference="profile:COGS:COG0438"
/inference="profile:PFAM:PF00534"
/inference="similar to AA
sequence:PIR:S64069"
/note="unnamed protein product;
Function: ALG2 of S. cerevisiae is
involved in N-glycosylation,
converting

```

```

man[2]glcnac-pp-dolichol to
man[3]glcnac-pp-dolichol. Title:
strong similarity to
mannosyltransferase Alg2 -
Saccharomyces cerevisiae"
/citation=[3]
/citation=[15]
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/db-xref="GI:134081897"
/db-xref="GOA:A2R3Y4"
/translation="MPPAKITIIHPDLGIGGAER
LIIDVALALQSRGHPVTIYTSHRD
KSHCFEEARDGTLDVQVRGNTIFPAHVGGRLFVL
MAILRQLHLTWDLTCGETTSGDNG
EGEEEVFIVDQMPACVPFLKVRKQRILFYCHFPD
QLLARDEGGSVLQLLKGLYRVPF
DWFEGWAVSASDKVVANSRFTRGVVSGVFGREKV
GDLSVVYPCVDTKAGDGGEGVVKD
GEKLWGGKKILLSVNRFERKKDLALAIRAYHGLG
EEKRKGTRLVVAGGYDNRVQENVQ
YHRELDELATGLGLQTATSKTVISALSIPDSIDV
LFLLSVPTAFRDTLLLQAKLLLYT
PINEHFGIVPVEAMRAGVPVLASNTGGPLETIVE
GETGWLRDAKVDADWTAVMDKVLV
GMKQEELDRMSVAAKERVEKEFSLTAMGEKLEQE
IEEMLGQEQRPFHGFQQLLTFLAL
VGVVLALAAFLVKLL"

exon      complement(181479..1820 /locus-tag="An14g05910"
86)

intron    complement(182087..1821 /locus-tag="An14g05910"
76)

exon      complement(182177..1826 /locus-tag="An14g05910"
01)

intron    complement(182602..1826 /locus-tag="An14g05910"
22)

exon      complement(182623..1829 /locus-tag="An14g05910"
90)

gene      complement(<183872..>18 /locus-tag="An14g05920"
9440)

mRNA      complement(join(<183872 /locus-tag="An14g05920"
..184411,
184472..188524,
188581..188756,
188813..189136,
189281..>189440))

CDS       complement(join(183872. /locus-tag="An14g05920"
.184411,184472..188524,
188581..188756,
188813..189136,
189281..189440))

/inference="profile:COGS:COG5059"
/inference="profile:PFAM:PF00225"
/note="unnamed protein product;
Function: kinesins are
microtubule-dependent motor
proteins, involved in organelle

```

transport, in mitosis and meiosis, and in the transport of synaptic vesicles along axons of animal neurons. Similarity: the closest homologues, comprising XCENP-E of *X. laevis*, are involved in driving congression of chromosomes to the metaphase plate. Similarity: the main feature of the predicted ORF is to contain, in the N-terminal half, several kinesin-like domains, explaining the strong similarity to several different kinesin-like proteins. Similarity: the predicted ORF has just half of the length of XCENP-E of *X. laevis*; the best homologue, having also a corresponding length, is a *N. crassa* hypothetical protein. Title: strong similarity to kinesin-related protein XCENP-E - *Xenopus laevis*"

/citation=[41]
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/db-xref="GI:134081898"
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MRTPRSTSRLSMSSRHGGGSRASD
EDGKTAVKVAVRVRPPLKPTDPGYELVPQRFQRP
MVHVTNPTSVAIDVPQGRKLFVFD
RVFAETVDQDGVWDYLSDSVSSFLQGYNVSI
LAY
GQSGAGKSYTMGTSGPSEQSDPRS
MGIIPRAAQLLFKLEGPAPKPNRNSGTGLRTPSR
YSVGSASSFGKASVEKNWQLKATY
VEIYNEQLRDLLVPESTHQGDRGTVTIREDAKGR
IILTGLHQVNINSYEDLMGALSFG
SSIRQTDSTAINAKSSRSHAVFSLNLVQRKASNG
VMSPTPKDKRMSMPVDMMSGSDAS
VMVDSKLHFVDLAGSERLKNTGASGERAKEG
ISINAGLAALGKVISQLSSRQAGAHVS
YRDSKLTRLQLQDSLGGNAYTYMIACVNP
AEFHLS
ETVNTVQYAQRARAIQSKPRIQQI
ADESDKHAVIERLKA EVAFLRQQLRNAEENG
RRS
AAPQDRAERQNEREVELQNQLLDT
QESYNALSQRHAKLISEIARDSEHAGETDP
NDV
SLVGKTSVERLKRSQSFAESIEQV
VLEYEKTIQSLESSLNTSSLSVTESTLLER
ET
KCAYVETVNSQLQARIQKLLDRES
STETYLHELEARLDGQSTGEEKQA AIVAE
LRKEL
SRARESEANCEDYISTLEERLAEA
DQDMELMQREMERLEHVIERQ RSLGKLDN
LLYEL
DHVQQNGNQKEQSEDELETHVPVP
AKGAYKPRTRATSLSLDVLTEAVETAIPES
DEGL
TEPAPEAVHEASVEAEATAETDET
NLKVLESATDRLEAQENGARASRASTPTQ
TKVVA
DKLETVTQELFDLRMQHESTVSEY
EMLEAKYAEAMKALAEFQRDAAD EARP
DEKVQD
LLSTNVESRPVSFLEEGKAPGSND
GKQPSSSPSLSSSEL SLAGEPASSHEQST
LSNGEV
PQENHVDTREIDEAKAQEVEQMRR
LLMEHQEGVSIMSQKYAQLQSEHEGTL
SLIETLK
AELQRSKNSSPPSTPGFKSPVIRR

KTSQSLIGTVDRAHRSLAALRNIAVEEFEARPDT
 MQNFEVHLDSAMHELHNRMERIQA
 LEAENQSVKKEMETKSTIISGLTRERSSLQGGGG
 SSVDMGLVNQLRDQVVQQENLINE
 MKESHDAREQLLAEIEELKSLKLTQEEAAKAQD
 LCAEEQERKISSLEGEVTELKSKH
 HNAVESLOSSEQELSATLAELDKALASIDAMRSE
 QTAAGEASASKDAAARELEAEREQ
 QEELVAKLKHVIDEHKATNAAHLEKIASLEKSHG
 EAQLQLSELLAAKDNDNSNEVQVHQ
 SRVSELEKEIDSHKSLADSFKKDLESLQESHKQE
 VTELEARATAAAQGDYESRFATMS
 AEHEEAMKTLRSEILESREELTKLLNMVSKLLNA
 DVTAEATMAEQIQEIMAQKHFSK
 YAEMLDTNEDLRKQLETKGSDEGRL
 EELMQSNSSKEAKVNELALLVATLEDTLQKEE
 QVKKKEAIIAEVKAKEKSVRLVEELEEQITNSF
 DQHHNRLSVIQQERDQALEDAKVK
 IAAYEKDIETYRVRIEQLEIKNQDSSSHDRSSSIT
 SNLRKSSSATSLSPPPAIPLPPL
 PTIASATNGTGSISPPSSRHTSKELVNPQIVDDQ
 EARIRTIEKHLNAEKQLTATLEEA
 LGDLEAQSNKVKSDCDAWKKKARELEEELTTLRK
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		/number=2
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		/number=3
exon	complement(188813..189136)	/locus-tag="An14g05920"
		/number=4
intron	complement(189137..189280)	/locus-tag="An14g05920"
		/number=4
exon	complement(189281..189440)	/locus-tag="An14g05920"
		/number=5
gene	complement(<190148..>191691)	/locus-tag="An14g05930"
mRNA	complement(join(<190148..190283, 190763..190861, 190948..191206, 191652..>191691))	/locus-tag="An14g05930"
CDS	complement(join(190148..190283,190763..190861, 190948..191206,	/locus-tag="An14g05930"

of *Eucalyptus grandis*. Title:
questionable ORF"
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/translation="MVECGMGVRAVVAFCDEREI
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LQKFMQYLSQRRITFGRISLSPGS
LAINEPLNPILWVMVLLIDRSVNRLGSRYSIIHF
SVLDNKAGRLCCYDDIGIMRFYSW
LQKCITSMEDLVYRIYIVGLVRNLHAMNVMCTLK
GWALPWIRSPTLNELYAFIASQLE
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HLWPEVE"

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		/number=1
exon	complement(192596..192700)	/locus-tag="An14g05940"
		/number=2
intron	complement(192701..192793)	/locus-tag="An14g05940"
		/number=2
exon	complement(192794..192853)	/locus-tag="An14g05940"
		/number=3
intron	complement(192854..192939)	/locus-tag="An14g05940"
		/number=3
exon	complement(192940..193251)	/locus-tag="An14g05940"
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		/number=4
exon	complement(193625..193690)	/locus-tag="An14g05940"
		/number=5
intron	complement(193691..193782)	/locus-tag="An14g05940"
		/number=5
exon	complement(193783..193884)	/locus-tag="An14g05940"
		/number=6
intron	complement(193885..193958)	/locus-tag="An14g05940"
		/number=6
exon	complement(193959..193985)	/locus-tag="An14g05940"
		/number=7
gene	complement(<194969..>196478)	/locus-tag="An14g05950"
mRNA	complement(join(<194969..195817, 195865..196221, 196455..>196478))	/locus-tag="An14g05950"
CDS	complement(join(194969..195817,195865..196221,	/locus-tag="An14g05950"


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196455..196478))
/note="Similarity: a short stretch
of amino acids of the predicted
ORF shows some weak similarity to
an A. thaliana hypothetical
protein."
/codon-start=1
/product="hypothetical protein"
/protein-id="CAK42156.1"
/db-xref="GI:134081901"
/translation="MFGTNRTDTPSVLYLTESL
MEIPCLSPAVADDIVPDLAQIFND
NPFKSLREQKISVPVLCGPHEQGPTDTHIDIFGQ
EFRTHSSLIKEYTGWIKERQRGEY
AERRVHYFEARTEKDGGWGIYRKGAVALTQPQRY
RDYPEIPDERIPSAIESFHCFLQA
LYLKPVVPYVGIGWRRMVLLGIRFQAVPRVREYI
EKIILPWTLTSTKPLLGLTDDILAY
TKMAQDIQCAQLYRECLIHLVGMAQYWGRNEFH
AEHILTPSAYASLIRHVGTVQRQLI
EKADVALHTFIRTLATQKPRRIPNFFLRQFTDTV
DNITGLNGRNMNSLGYYQHIRLVL
NDMQLRIPRGSTYNMCHRLWQFIGCLCVNGLLYT
QDQIKGYPVCISPTDIELPWVLAN
APEAPVEDQVRDAIMEG"
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17)
/number=1
intron    complement(195818..1958 /locus-tag="An14g05950"
64)
/number=1
exon      complement(195865..1962 /locus-tag="An14g05950"
21)
/number=2
intron    complement(196222..1964 /locus-tag="An14g05950"
54)
/number=2
exon      complement(196455..1964 /locus-tag="An14g05950"
78)
/number=3
gene      complement(<197258..>19 /locus-tag="An14g05960"
8879)
mRNA      complement(join(<197258 /locus-tag="An14g05960"
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197402..197552,
197606..197698,
197751..197968,
198017..198238,
198288..198371,
198435..198525,
198598..198694,
198745..>198879))
CDS       complement(join(197258. /locus-tag="An14g05960"
.197342,197402..197552,
197606..197698,
197751..197968,
198017..198238,
198288..198371,
198435..198525,
198598..198694,
198745..198879))
/EC-number="3.5.3.11"

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/inference="profile:COGS:COG0010"
/inference="profile:PFAM:PF00491"
/note="unnamed protein product;
Catalytic activity: H2O + agmatine
<=> urea + putrescine. Complex:
agmatinase of E. coli is a
homodimer of the speB gene
product. Function: agmatinase of
E. coli is part of the second
putrescine biosynthetic pathway;
it also represents the only
pathway for urea biosynthesis in
E. coli as no urease is present.
Similarity: the predicted ORF
shows much stronger similarity to
putative agmatinases of N. crassa
and S. pombe. Title: strong
similarity to agmatinase speB
-Escherichia coli"
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HDQTPLAGPHQRLWYNTLPGDGGT
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APFDTGTSYRPGARFGPSGIRQGS
RRLNLYGGYNVPLQANPFVSDLRVLD CGDIPVTS
YDNAWAIQQIEEGHNSVLMRKPFT
DAEKYGLSKAGKTLPRIITLGGDHTITLPLLRSI
NRAYGPVTVIHFDSHLDSWKPKVF
GGSPSQVAAINHGTYFYHAAMEGLLKNDTNIHAG
IRTTLSGSPSDYENDGYCGFEIVEA
REIDTIGTDGIIKKIRERVGTENPVYLSIDIDTL
DPAYAPATGTPETGGWSTRELRTI
IRGLDGLNFIGADIVEVAPAYDTNAELSTMAAAD
VLYEVLTIMVKKGPLSVGRSDEL"
sig-peptide      complement(198823..1988 /locus-tag="An14g05960"
79)
mat-peptide      complement(join(197261. /inference="protein
.197342,197402..197552, motif:SignalP:2.0"
197606..197698, /locus-tag="An14g05960"
197751..197968,
198017..198238,
198288..198371,
198435..198525,
198598..198694,
198745..198822))
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42) /locus-tag="An14g05960"
intron            complement(197343..1974 /number=1
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exon              complement(197402..1975 /number=1
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mRNA	complement(join(<199830..200758, 200827..>201412))	/locus-tag="An14g05970"
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		/inference="profile:PFAM:PF01554"
		/inference="similar to AA sequence:PIR:T37517"
		/note="unnamed protein product; Title: strong similarity to hypothetical protein SPAC11D3.06 - Schizosaccharomyces pombe"
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		/translation="MYDSLPSYRETSSAHTHEE"

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 LGGTTALDTLASSTFTGSSNKHDLGILLQRAFFV
 LGLFYVPVAILWTCSEPVFLLLGQ
 DPQLSRDSARFLTCLIPGGLGYIYFEAMKKYLQA
 QGIMRPGTYVLLITVPFNALLNYL
 FCYTFRMGLLGAPFATGISYWLSFALLVLYARFI
 AGSECWGGWSRKAFENLGT FARLA
 FLGVVHVGT EW WAFEIVALAAGRLGTIPLAAQSV
 IMTADQVLNTIPFGVG VATSSRVG
 SLLGSRDAAGASRAANTAAWLSMALGGAVLAVLM
 GTRHVF AKIFNSDEGVVQLTAEVL
 PWVALFQIADGLNGSCGSLRGMGRQHVGALVNL
 ASYYCGALPLGIWLA FN GWGLKGL
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intron	complement(200759..200826)	/locus-tag="An14g05970"
		/number=1
exon	complement(200827..201412)	/locus-tag="An14g05970"
		/number=2
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mRNA	join(<202677..203229, 203273..203374, 203431..>204146)	/locus-tag="An14g05980"
CDS	join(202677..203229, 203273..203374, 203431..204146)	/locus-tag="An14g05980"

/inference="profile:COGS:COG0477"
 /inference="similar to AA
 sequence:PIR:S61140"
 /note="unnamed protein product;
 Function: TPO3 of S. cerevisiae is
 a vacuolar polyamine transporter,
 that controls the cytoplasmic
 spermine content. Phenotype: S.
 cerevisiae cells in which TPO3 was
 disrupted showed an increased
 sensitivity to polyamine toxicity
 and a decrease in polyamine uptake
 activity and polyamine content in
 vacuoles. Phenotype: S. cerevisiae
 cells overexpressing TPO3 were
 resistant to polyamine toxicity
 and showed an increase in
 polyamine uptake activity and
 polyamine content in vacuoles.
 Remark: TPO3 of S. cerevisiae is
 also called YPR156c or P9584. 7.
 Similarity: the predicted ORF is
 125 amino acids longer at the
 N-terminus than TPO3 of S.
 cerevisiae. Title: strong
 similarity to polyamine transport
 protein Tpo3 - Saccharomyces
 cerevisiae"
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		<pre> /protein-id="CAK42159.1" /db-xref="GI:134081904" /translation="MNLKLTQIDLVPVPEKQSAS DIDSLPVEQHGTHTHPAPTS DPLD PLNWPRWRKHVILGIVMLKFVLPEQSRRLHRLTM NRYFLFTYITTTTVPSFAEIQSQY DINYSQVNWTVAIPALGLSLGPLFWSSVGDIIYGR RIVFIVGTVIALVATIGAAVADTY GGYMAARFFQGFVSPSSTVGMVANGTVTDMFY EYERGQKLGLWVLALDSGLLLGPT FGGFLNLVSAQWINWFNAILFAALLLLELTLMPE TLYPRALMLQRMVTEKPAESNAG IEEAGIKRTKSLPFFNLRPIPGLSHPPIYASLTR FLLTFRFPVIAVAVIGYSFTWYWW ILSVITMVPSAYATDSPLIQGLLFLGLLIGTLVA EVSCSGRLSDAIVGRLAKRNGGVR VPEMRLWLAYPAIVLTAGVYIPIAHVRTISNIAI QPAVGLILWGISIDKAYHWMVGQV AFFLCE" </pre>
exon	202677..203229	<pre> /locus-tag="An14g05980" /number=1 </pre>
intron	203230..203272	<pre> /locus-tag="An14g05980" /number=1 </pre>
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exon	203431..204146	<pre> /locus-tag="An14g05980" /number=3 </pre>
gene	complement(<205094..>207843)	<pre> /locus-tag="An14g05990" </pre>
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CDS	complement(join(205094..207273,207361..207431, 207517..207554, 207700..207843))	<pre> /locus-tag="An14g05990" /note="unnamed protein product; Title: weak similarity to spindle pole body-associated protein sadlp - Schizosaccharomyces pombe" /codon-start=1 /protein-id="CAK42160.1" /db-xref="GI:134081905" /translation="MRNLVYPKYHVLESLNRPCD AVDRHSTRVFSRRVAFALEGRQLP RIAIDTSELVILVAAIVALASPALDLCRLQASY SVPSSHTNRNIKPILLRIELPMPA RRGATRRAGSTRSDIGSASTYFQSKLGPEARTQA LPNLPTKQSFAYGSAETPILPREL KIQPHMDLTEMADAIDKGIEDAKDRQMKEKETQ DKSRRQKSPSITRSPVRRSRREPT PDELQLLDNLREATKSPTPVRGNYSNNDQSTATP TPPIPHTLSTASSPAQSLPVPRYP HVPAENLYPSPMGRFGPQLHDGPPLGSSPLPDDS SLYSFTVERAINSDELTRTLSDGK NIKAPPRRFSGLAFANEPHHEEEEPDSRLLKTKS RSPSLQPSYEDFQIEPSPEPEPQS EPESVQELELEPTPEPEPIPELEPMPEPTPEPEV IREKSPAAQFTAPTCTLIPNAYAR </pre>

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AQVSSLAKEMRTVKWDVNEVQSEV
RSSPTPIMPSPRGSTD LGPPT EQKTNFLSIGLGV
IVIPGLTSPTVGHKLSAQWAYVN
LWRGSHYRPASPPLAALVPWEDYGDCWCSTPRDG
MSQIGIDLGQKIVPEEVAVEHMPK
TATLKPENAPREMELWAQYVLVQKTSRPARTQA
ERFSIHKPIMDALRSAWPTEDPTA
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31)
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16)
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exon      complement(207517..2075 /locus-tag="An14g05990"
54)
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99)
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exon      complement(207700..2078 /locus-tag="An14g05990"
43)
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gene      complement(<208451..>21 /locus-tag="An14g06000"
0658)
mRNA      complement(join(<208451 /locus-tag="An14g06000"
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208778..209568,
209634..209834,
209889..210489,
210572..>210658))
CDS       complement(join(208451. /locus-tag="An14g06000"
.208726,208778..209568,
209634..209834,
209889..210489,
210572..210658))

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/inference="profile:PFAM:PF00400"
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sequence:PIR:S56893"
/note="unnamed protein product;
Function: MDV1 of S. cerevisiae is
involved in the mitochondrial
membrane fission event by
regulating the assembly of Dnm1p,
a dynamin-related GTPase, into
punctate structures at the outer
mitochondrial membrane. Phenotype:
the mitochondrial fission is
blocked in S. cerevisiae MDV null

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mutants and mitochondrial
 membranes form nets. Remark: is
 also called YJL112w, NET2, FIS2 or
 GAG3. Title: strong similarity to
 mitochondrial fission protein Mdv1
 - *Saccharomyces cerevisiae*"
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 SRAISSLPDELLANIPDDSSSYSLFQGFQASQDD
 IEYRRARRRRSSKSKKLLKDGETR
 GALPSAPSDLKKERD LLSRRMELMGVRKNMCSSE
 IHDIDNKIANLHNMRKIVLDRLAG
 LEMEEADLEHELNEIENKLEDIQEEQQEAEVPPP
 ATPKSSEANDDSIVSEDPAMGASF
 MSESIIYQKIPSPKSVKQRSIILHEHFAPGSEIKE
 MPAHSDMVT AIDFDY PFGTMISAA
 LDDTVRVWDLNVGRCVGFLEGHNASVRCLQIEDN
 IVATGSM DASVKLWDL SRARTTTR
 DNRVTRREDDEESAQADDASMASHSTTLED CYVY
 SLDAHVDEV TALHFKGDTLISGSA
 DKTLRQWDLVKGR CVQTL DVLWAAAQASTLGSET
 TWRPSGRLPDASAD FVGAVQCFDA
 ALACGTADGMVRLWDLRSGQVHRSLVGHTGPITC
 LQFDDVHLVTGSQDRSIRI WDLRT
 GSIFDAYAYDKPITSMMFDTKRIVAAAGENVVKV
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exon	complement(209634..209834)	/locus-tag="An14g06000"
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intron	complement(209835..209888)	/locus-tag="An14g06000"
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intron	complement(210490..210571)	/locus-tag="An14g06000"
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exon	complement(210572..210658)	/locus-tag="An14g06000"
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mRNA	join(<211445..211515, 211743..212394, 212451..>212528)	/locus-tag="An14g06010"
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exon	211445..211515	/locus-tag="An14g06010"
intron	211516..211742	/number=1 /locus-tag="An14g06010"
exon	211743..212394	/number=1 /locus-tag="An14g06010"
intron	212395..212450	/number=2 /locus-tag="An14g06010"
exon	212451..212528	/number=2 /locus-tag="An14g06010"
gene	complement(<212729..>21 3754)	/number=3 /locus-tag="An14g06020"
mRNA	complement(join(<212729 ..213283, 213342..213578, 213671..>213754))	/locus-tag="An14g06020"
CDS	complement(join(212729. .213283,213342..213578, 213671..213754))	/locus-tag="An14g06020"

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		/note="Remark: the predicted ORF is only 45 amino acids long." /codon-start=1 /product="hypothetical protein" /protein-id="CAK42164.1" /db-xref="GI:134081909" /translation="MPFAQNGDAVTKADYQVEEG IKYLREVKTTLHPFVVKAPSVGSY T"
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intron	214445..214505	/locus-tag="An14g06030"
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exon	214506..214606	/locus-tag="An14g06030"
		/number=2
gene	complement(<216128..>217084)	/locus-tag="An14g06040"
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CDS	7084) complement(216128..217084)	/locus-tag="An14g06040" /inference="profile:COGS:COG0599" /inference="similar to AA sequence:PIR:T39714" /note="unnamed protein product; Similarity: the predcited ORF is 96 amino acids longer at the N-terminus than the hypothetical protein SPBC17D11. 03c of S. pombe. Title: weak similarity to hypothetical protein SPBC17D11.03c - Schizosaccharomyces pombe" /codon-start=1 /protein-id="CAK42165.1" /db-xref="GI:134081910" /translation="MARNPSRLLPPSRSLQLTTS KRQFGTGASILPLLSPPRYRPLRS SLISSTPSSSPLAHRIPTFATPLRTITTSSNSAP TKMTTITIDPKYAQLFQSLESQFQT TTLPHDKWYILAISTLVANPDPERADQLYLYLTS KPEYSTPSSRQDLIRRIREALIKS VIIVGVCKPIEAILAISKLEAPEDKDYFTFTRENW QCDEANHERGVAVLEKLYARNTSG TLDLFAAHKDFAWLSKEITYGLFLSDRGVLDLDDLD TQLVVLPAIMSQNLKIETHWHIRG TRRLGVSLDVDVRVLCCEGVKHVAGFYGRVLDKVP VEEVEGDV"
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exon	217593..217931	/locus-tag="An14g06050"
intron	217932..218002	/number=1 /locus-tag="An14g06050"
exon	218003..218104	/number=1 /locus-tag="An14g06050"
gene	complement(<218542..>219708)	/number=2 /locus-tag="An14g06060"
mRNA	complement(<218542..>219708)	/locus-tag="An14g06060"
CDS	complement(218542..219708)	/locus-tag="An14g06060"

/inference="similar to AA
 sequence:UniProtKB:SC05211.1"
 /note="unnamed protein product;
 Function: TTP1 of *S. cerevisiae* is
 involved in the transfer of
 mannose residues to the mannans of
 glycoproteins during maturation in
 the Golgi. Function: the correct
 mannosylation of proteins by TTP1
 of *S. cerevisiae* is essential for
 growth and morphogenesis. Golgi
 Phenotype: the N-linked sugar
 residues in the *S. cerevisiae* TTP1
 null mutant lack the main
 alpha-1,2-linked branches of the
 mannan. Remark: TTP1 of *S.*
cerevisiae is also called *mn2* or
YBR015C. Title: strong similarity
 to alpha-1,2-mannosyltransferase
 Ttp1 - *Saccharomyces cerevisiae*"
 /citation=[43]
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 FAVLFSSFEVVIWMDADCFPLHKPEVLLSEPF
 SKGLVTWPDFWISSASPLYFTISR
 QEMPALSERASSEAGVFLVSKKTHQMTLLLAAYY
 NYYGPSHYFRLLSQGAPGEGDKET
 FLHAASAVGEPFYAVSERVQAVGHTKPGGIAGSA
 MVQTDPAEDYALTSAGKWRVQDES
 VAKAPRAFFIHANYPKFNPGEKVFGMKWETTPTL
 RPDGTDGRAWLVAESTVQRFGYDV
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exon	complement(218542..219708)	/locus-tag="An14g06060"
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gene	<221804..>226148	/locus-tag="An14g06070"
mRNA	join(<221804..221887, 221930..224173, 224489..224622, 224729..224737, 224926..224987, 225102..225280, 225490..225530, 225672..225708, 225858..225905, 225959..225993, 226055..>226148)	/locus-tag="An14g06070"
CDS	join(221804..221887, 221930..224173, 224489..224622, 224729..224737, 224926..224987, 225102..225280, 225490..225530,	/locus-tag="An14g06070"

225672..225708,
225858..225905,
225959..225993,
226055..226148)

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sequence:UniProtKB:NCB7F21.6"
/note="unnamed protein product;
Title: similarity to hypothetical
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crassa"
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QPAVAPPKLP RATGPRAVSKSQPA
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220741	ccaccgaacc	gacagagtgg	aaagtggaa	ggaaagtcca	ccagtggatc	ccattagctt
220801	ggtctaccga	aaccttaaga	agttaagggg	aatctggaat	cttggatcga	ctgagaaggg
220861	aagactggga	gaaggaggga	gagggagagg	aatgaggaat	gagatcctcg	gctcgaggag
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220981	tttttgtggc	ttgttacatt	gaagaaggac	aatgcaactg	cccgtagtgc	ctgttccggc
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221101	aactacttga	actacttgaa	ctgctttag	gatatctcat	ctgtgcaccg	agtcgagttc
221161	gtcacgccaa	ctctgcaatc	tgcagctgcg	actctgcacc	ggctatgaac	tgttcttctc
221221	cctctgggtc	catctgaaac	gggtggctcaa	tttcgcccgc	actcggccgc	catcaagtaa
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221461	gcgaactaga	tccatccccg	atgtgtttcg	attataaacg	accgtaagcg	tggtcctccg
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221701	ccacttatgg	gaccccgcac	tccgggttat	ctccacattg	tttgctgga	ccagttagta
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221821	ggctcgaatc	cgcaaaactc	cgccgggtctc	cgccccagct	ccccgaaaa	ggcgtaggag
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222001	caagacagcg	ttgacatggg	gcgtaggagt	tgccagtcgg	ggaaagcttc	gaggattgtc
222061	cctccccgtg	accggggcac	agcctgcggg	cgcacccccg	aagcttcccc	gtgcgacagg
222121	tccacgagca	gtgtccaaat	cgcaaccggc	tcttgacaca	gcccgcagaaa	aacgacgact
222181	tcatgataag	cagcgttcat	cagccgcggg	gcttacagag	catgggtctg	tctcgattcc
222241	acctacttca	caacgccgct	tgtgctcacc	ggagtactac	actgtggatt	cccatgttaa
222301	gccgaatcac	cataatcctt	attcttcacg	tgcgacaaa	accgattctt	tgaacaata
222361	ccatgcccc	ttggctcgaa	accccgattc	atcaagggcc	tggatgggg	tagaacagac
222421	accggtaccg	atacagtgtc	cgtggccagc	cctgactccg	gaacagaaa	ataatgcttc
222481	ggatgagcaa	catgaagaaa	cctcttataa	cgaggtttca	ccacgtatga	gtgcttgcca
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222601	atacctaatt	agttattatg	ccgaagtcac	tgtccgatg	attgtggcat	ttgatagtcc
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222721	agccatcgcg	acgttggcaa	gctgcaatct	gcgacagcga	cgcgaacgag	gcacgaggtc
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222841	agcattacag	gaccggaccg	gtatctttat	gcctgaagat	tatgccagg	aagagcagta
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222961	ttcagactcc	gtcctggcga	ccttactcat	cctctgtcta	ttccacgggt	gtgatactgg
223021	ggtggctcaa	ttcaagacct	agtttgccgg	ggtgacaaaa	ttggtggcta	ttcgactgtg
223081	caactcacct	tgcattgtcg	atgaactgaa	gtgggttgtt	cgcattgttc	catggattga
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223321	cacatctacg	ccaccagaca	tccatatacc	atccactact	ctcccgccct	cgatggcggt
223381	cttcccacg	aacattccag	ccacctcgtc	cggtcctttt	gcatttacct	tgccgccgct
223441	gccgcctcct	ggtgatcgcg	acagaggaca	gctgccgccg	gcgttctggg	ctgaatggta
223501	ttctctccga	cagaagcttg	agtcctggcg	atttgttccc	caccaatcgc	agtcacagtc
223561	acctctcttt	acatccagcc	acgcctacat	ctcgccacct	tcatcgccga	cagaccagcc
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223681	ggcgatcttg	tacgcgagc	gactgccta	tccagacctc	ccgtccgac	acctcgtat
223741	tcaaaacatt	gtgcaacaca	taatgagtc	cattatgacc	gttcaatctg	acgcgtatct
223801	cctgtggcca	ctattcatca	ccgggtcgga	gtgcgtgcgt	gccgatcatc	gcgccattat
223861	ccgccaacgg	tgcaaagatc	tatccaggga	ctctgggttc	ttcaacaacc	tctcatgctt
223921	gcagctcctg	gagaagatct	gggcagagaa	ccctgccgtg	gatgtgatcc	ctgttgtctc
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224101	tgtctctcgg	aagcagggat	tccgctggca	cgaggcgatg	caaaccaaa	gcgcggagga
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224341	acctgaacct	tcggggccaca	acaggccccc	actatcgga	ccatcgcact	agatccgttc
224401	ccacttccca	cacaatccgc	tcgatacgt	ccatcacgac	agtaccctac	tgcgtaaaat
224461	tctccgtaaa	cctactgtca	tctgtcagaa	ctccatcgat	gatgcattca	ctccatctgg
224521	tccctctagc	aacctgcctc	accagcccac	caaacaac	cacaaaagta	gcggcaccgg
224581	gcatctcccg	agcgccagta	cgtcggaaaa	tttgtgttgg	aggtgagttg	agtttcgggt
224641	ctgcgtgtca	gatgctcatt	tgtgggtgtt	ggactctgag	aggtgtcca	cccatcactt
224701	agatagtact	gtgccgctgt	ggtgatagaa	tgagtgggta	agtaattgcc	taactcttgg
224761	agagaagggg	tcttggtcac	tttgtttctt	gaattactgg	tttgggtatg	cggagggggg
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224941	tggcagtgac	ggtatcgcca	ctggtggact	aaatattact	atctatagtt	agtattagat
225001	cccactaata	gtgaacgctc	atgcacatag	ccatgctctc	tctctacatt	attaactaac
225061	cacatagtta	atactatact	acatcttaaa	taataacctc	gtcagatttc	gtcatcccca

225121 tcaccggata gatggaagga agatagaaac ccacaagcgt atcgctaagc gtgactctga
 225181 ctcgtctcca caagacaaga gaacagattt gcaacgtgac ccaaacttac ttttactttt
 225241 gcggatagaa gatgaggggt tcactttaca tcatcaacta gtacacatac agtaatcaac
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 225361 gataatgcca atgtgatagt gatgagattc atcaccttcg gcggctattc ggggggtctta
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 226501 tta

L5 ANSWER 26 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AE014133 GenBank (R)
 GenBank ACC. NO. (GBN): AE014133 AE014853-AE015037
 GenBank VERSION (VER): AE014133.1 GI:24378526
 SEQUENCE LENGTH (SQL): 2030921
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 24 Jan 2006
 DEFINITION (DEF): Streptococcus mutans UA159, complete genome.
 SOURCE: Streptococcus mutans UA159
 ORGANISM (ORGN): Streptococcus mutans UA159
 Bacteria; Firmicutes; Lactobacillales;
 Streptococcaceae; Streptococcus

COMMENT:

On or before Jan 18, 2006 this sequence version replaced
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 gi:24378472, gi:24378487, gi:24378500, gi:24378511, gi:24378520.

REFERENCE: 1 (bases 1 to 2030921)
 AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;
 Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;
 Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;
 Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.
 TITLE (TI): Genome sequence of Streptococcus mutans UA159, a
 cariogenic dental pathogen
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (22), 14434-14439
 (2002)
 OTHER SOURCE (OS): CA 137:364100
 REFERENCE: 2 (bases 1 to 2030921)
 AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;
 Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;
 Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;
 Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (09-JUL-2002) Department of Microbiology and
 Immunology, University of Oklahoma Health Sciences
 Center, 940 SL Young Blvd., Oklahoma City, OK 73104,
 USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2030921	/organism="Streptococcus mutans UA159" /mol-type="genomic DNA" /strain="UA159" /db-xref="taxon:210007"

L5 ANSWER 27 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): BX571856 GenBank (R)
 GenBank ACC. NO. (GBN): BX571856
 GenBank VERSION (VER): BX571856.1 GI:49240382
 CAS REGISTRY NO. (RN): 726687-34-9
 SEQUENCE LENGTH (SQL): 2902619
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 7 Oct 2006
 DEFINITION (DEF): Staphylococcus aureus subsp. aureus strain MRSA252,
 complete genome.
 KEYWORDS (ST): complete genome
 SOURCE: Staphylococcus aureus subsp. aureus MRSA252
 ORGANISM (ORGN): Staphylococcus aureus subsp. aureus MRSA252

REFERENCE: Bacteria; Firmicutes; Bacillales; Staphylococcus
 1 (bases 1 to 2902619)
 AUTHOR (AU): Holden,M.T.; Feil,E.J.; Lindsay,J.A.; Peacock,S.J.;
 Day,N.P.; Enright,M.C.; Foster,T.J.; Moore,C.E.;
 Hurst,L.; Atkin,R.; Barron,A.; Bason,N.; Bentley,S.D.;
 Chillingworth,C.; Chillingworth,T.; Churcher,C.;
 Clark,L.; Corton,C.; Cronin,A.; Doggett,J.; Dowd,L.;
 Feltwell,T.; Hance,Z.; Harris,B.; Hauser,H.;
 Holroyd,S.; Jagels,K.; James,K.D.; Lennard,N.; Line,A.;
 Mayes,R.; Moule,S.; Mungall,K.; Ormond,D.; Quail,M.A.;
 Rabbino-witsch,E.; Rutherford,K.; Sanders,M.; Sharp,S.;
 Simmonds,M.; Stevens,K.; Whitehead,S.; Barrell,B.G.;
 Spratt,B.G.; Parkhill,J.
 TITLE (TI): Complete genomes of two clinical Staphylococcus aureus
 strains: evidence for the rapid evolution of virulence
 and drug resistance
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 101 (26), 9786-9791
 (2004)
 OTHER SOURCE (OS): CA 141:152000
 REFERENCE: 2 (bases 1 to 2902619)
 AUTHOR (AU): Holden,M.T.G.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (23-JUN-2004) Submitted on behalf of the
 Pathogen Sequencing Unit, Sanger Institute, Wellcome
 Trust Genome Campus, Hinxton, Cambridge CB10 1SA,
 E-mail: mh3@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..2902619	/organism="Staphylococcus aureus subsp. aureus MRSA252" /mol-type="genomic DNA" /strain="MRSA252" /sub-species="aureus" /db-xref="taxon:282458"

=> d 15 20

L5 ANSWER 20 OF 27 USPATFULL on STN
 AN 2003:71519 USPATFULL
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
 Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
 Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
 Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF
 PI US 20030049804 A1 20030313
 AI US 2000-746660 A1 20001222 (9)
 RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
 PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
 2000, PENDING
 PRAI DE 1999-19931420 19990708
 US 1999-141031P 19990625 (60)
 US 1999-142101P 19990702 (60)
 US 1999-148613P 19990812 (60)
 US 2000-187970P 20000309 (60)

DT Utility
 FS APPLICATION
 LN.CNT 15004
 INCL INCLM: 435/115.000
 INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200
 NCL NCLM: 435/115.000
 NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200
 IC [7]
 ICM C12P013-08
 ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21
 IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
 C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
 C12N0001-21 [ICS,7]
 IPCR C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
 C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
 C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
 C12N0009-90 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 21

L5 ANSWER 21 OF 27 USPATFULL on STN
 AN 2003:95966 USPATFULL
 TI Polynucleotides, materials incorporating them, and methods for using
 them
 IN Glenn, Matthew, Auckland, NEW ZEALAND
 Havukkala, Ilkka J., Auckland, NEW ZEALAND
 Bloksberg, Leonard N., Auckland, NEW ZEALAND
 Lubbers, Mark W., Palmerston North, NEW ZEALAND
 Dekker, James, Palmerston North, NEW ZEALAND
 Christensson, Anna C., Lund, SWEDEN
 Holland, Ross, Palmerston North, NEW ZEALAND
 O'Toole, Paul W., Palmerston North, NEW ZEALAND
 Reid, Julian R., Palmerston North, NEW ZEALAND
 Coolbear, Timothy, Palmerston North, NEW ZEALAND
 PA Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.
 corporation)
 Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.
 corporation)
 PI US 6544772 B1 20030408
 AI US 2000-634238 20000808 (9)
 DT Utility
 FS GRANTED
 LN.CNT 2015
 INCL INCLM: 435/252.300
 INCLS: 435/320.100; 536/023.700
 NCL NCLM: 435/252.300
 NCLS: 435/320.100; 536/023.700
 IC [7]
 ICM C12N001-21
 ICS C12N015-63; C12N015-31
 IPCI C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]
 IPCR A23C0019-00 [I,C*]; A23C0019-032 [I,A]; C07K0014-195 [I,C*];
 C07K0014-335 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
 C12N0015-31 [I,C*]; C12N0015-31 [I,A]
 EXF 435/252.3; 435/320.1; 536/23.7
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 22

L5 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN
 AN 1999-00562 BIOTECHDS
 TI Use of lactic and propionic acid bacteria;
 to bind mycotoxin to prevent their absorption or to purify
 contaminated food or feedstuff
 AU El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J
 PA Roy.Melbourne-Inst.Technol.
 LO Melbourne, Victoria, Australia.
 PI WO 9834503 13 Aug 1998
 AI WO 1998-AU63 6 Feb 1998
 PRAI AU 1997-5005 7 Feb 1997
 DT Patent
 LA English
 OS WPI: 1998-557001 [49]

=> d hist

(FILE 'HOME' ENTERED AT 13:55:21 ON 07 JUL 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
 AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
 CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
 DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:55:47 ON 07 JUL 2008
 SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELL? AND

 0* FILE ADISCTI
 SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELLS

0* FILE ADISCTI
 SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND?

0* FILE ADISNEWS
 0* FILE ANTE
 0* FILE AQUALINE
 0* FILE BIOENG
 1* FILE BIOTECHABS
 1* FILE BIOTECHDS
 0* FILE BIOTECHNO
 2 FILE CAPLUS
 0* FILE CEABA-VTB
 0* FILE CIN
 0* FILE ESBIODBASE
 0* FILE FOMAD
 0* FILE FOREGE
 2* FILE FROSTI
 0* FILE FSTA
 5 FILE GENBANK
 1 FILE IFIPAT
 0* FILE KOSMET
 0* FILE NTIS
 0* FILE NUTRACEUT
 1* FILE PASCAL
 0* FILE PHARMAML
 1 FILE SCISEARCH
 1 FILE TOXCENTER
 21 FILE USPATFULL
 3 FILE USPAT2
 0* FILE WATER
 2 FILE WPIDS
 2 FILE WPINDEX

L1 QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?

FILE 'BIOTECHDS, CAPLUS, FROSTI, GENBANK, IFIPAT, PASCAL, SCISEARCH,
TOXCENTER, USPATFULL, USPAT2' ENTERED AT 13:59:37 ON 07 JUL 2008

L2 38 S L1
L3 34 DUP REM L2 (4 DUPLICATES REMOVED)
L4 27 S L3 AND (TABLET OR FOOD OR DIETARY SUPPLEMENT OR CONFECTIONERY
L5 27 DUP REM L4 (0 DUPLICATES REMOVED)

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	174.83	178.94

STN INTERNATIONAL LOGOFF AT 14:06:30 ON 07 JUL 2008